

Db	301	CAAAATTGACGTCATGGAATTGGGTCAGAAAACAATGCTCTCTTGAGCTTGACAT	360
Qy	361	GAAGTGAATGTCAGTCATGAGTCACACTGATCCGATCTGTATATATATGCCAAATAGCTA	420
Db	361	GAAGTGAATGTCAGTCATGAGTCACACTGATCCGATCTGTATATATATGCCAAATAGCTA	420
Qy	421	CACGCAACATTACAAACAACCCCATCTACTATACATCACAAAGTTTGTTCATGAATAAAC	480
Db	421	CACGCAACATTACAAACAACCCCATCTACTATACATCACAAAGTTTGTTCATGAATAAAC	480
Qy	481	AAATTAAGTATGACGAGAGGGGACAAATPAATCTTTGCTTGACGCGTAAAGTAAATTACAAAG	540
Db	481	AAATTAAGTATGACGAGAGGGGACAAATPAATCTTTGCTTGACGCGTAAAGTAAATTACAAAG	540
Qy	541	CCATATATCAACCTTATCTATCTATTAATAAGTTTCGTATATATATACGACGATGATCTCAA	600
Db	541	CCATATATCAACCTTATCTATCTATTAATAAGTTTCGTATATATATACGACGATGATCTCAA	600
Qy	601	CAACCGTACTGTGTAAGGCAACAAATATAGCCACGCAAAAAATGCAGAAATGATCATAT	660
Db	601	CAACCGTACTGTGTAAGGCAACAAATATAGCCACGCAAAAAATGCAAAATGATCATAT	660
Qy	661	GATGACGAACGTACACTCTGGCTTGCTACATPAAGTGAATGATGATGATCATPAATATTTGGC	720
Db	661	GATGACGAACGTACACTCTGGCTTGCTACATPAAGTGAATGATGATGATCATPAATATTTGGC	720
Qy	721	AAGAAACCGTGAAGACTACACAGCCGTGCTCACTAGTACAGACAGGAACAAGAAATCTGTCT	780
Db	721	AAGAAACCGTGAAGACTACACAGCCGTGCTCACTAGTACAGACAGGAACAAGAAATCTGTCT	780
Qy	781	AATCGAAGCTATPAATAAACCCCTAGTATGCTTATGCACTTCTCCATCAGCCTACCCATAT	840
Db	781	AATCGAAGCTATPAATAAACCCCTAGTATGCTTATGCACTTCTCCATCAGCCTACCCATAT	840
Qy	841	CTTCAGTCTATTACTCTTCTCTATCTACTCTCAGAGAGCAGAGAAATGCGACACC	894
Db	841	CTTCAGTCTATTACTCTTCTCTATCTACTCTCAGAGAGCAGAGAAATGCGACACC	894
RESULT 2			
US-09-078-972A-19			
Sequence 19, Application US/09078972A			
Patent No. 6635806			
GENERAL INFORMATION:			
APPLICANT: KRIS, ALAN L.			
APPLICANT: LUETHY, MICHAEL H.			
APPLICANT: VOYLES, DALE A.			
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EXPRESSION OF TRANSGENES			
TITLE OF INVENTION: IN PLANTS			
FILE REFERENCE: DEKM:158			
CURRENT APPLICATION NUMBER: US/09/078,972A			
CURRENT FILING DATE: 1998-05-14			
NUMBER OF SEQ ID NOS: 28			
SOFTWARE: PatentIn Ver. 2.0			
SEQ ID NO 19			
LENGTH: 412			
TYPE: DNA			
ORGANISM: Artificial Sequence			
FEATURE:			
OTHER INFORMATION: Description of Artificial Sequence: Synthetic			
US-09-078-972A-19			

Query Match	46.0%;	Score 411;	DB 4;	Length 412;
Best Local Similarity	100.0%;	Pred. No. 3,38-118;		
Matches 411;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
OY	484	TAAGTATGACGAGGGGACAATTAATCCTTGTGACGGCTAAAGTAATTACAAAGCA	543	
Db	2	TAAGTATGACGAGGGGACAATTAATCCTTGTGACGGCTAAAGTAATTACAAAGCA	61	
OY	544	TATATCAACCTATATCTTAATTAATAGTTCGTTATATATAGCGACGATGATCATCAACA	603	

Db	62	TATATGACCTATATCTAATTAAAGTTGGTAAATATACGACGATGATCATCAAA	122
Oy	604	CGTACCTGTGAAAGGCACAAATGAGCCACGCAAAATGACAAATGATCCATATGAT	663
Db	122	CGCTACCTGTGAAAGGCACAAATGAGCACGCAAAATGACAAATGATCCATATGAT	181
Oy	664	GACGAACGTACACTCGGCTTGTCTACATAAGTGAATGATGATCAATTAATTGGCAG	723
Db	182	GACGAACGTACACTCGGCTTGTCTACATAAGTGAATGATGATCAATTAATTGGCAG	241
Oy	724	AAACCGTAAAGCTACACAGCGCTGTGATGACACAGGAACAAAGAAACTGTGCTAAT	783
Db	242	AAACCGTAAAGCTACACAGCGCTGTGATGACACAGGAACAAAGAAACTGTGCTAAT	301
Oy	784	CGAAGCTATAAATAAACCTAGTATGCTATGACATCTTCATCAACAATAACCATATCTT	843
Db	302	CGAAGCTATAAATAAACCTAGTATGCTATGACATCTTCATCAACAATAACCATATCTT	361
Oy	844	CAGCTAATTACCTTCTCTATCTACTCCAGAGAGACAGGAAGATCGACACC	894
Db	362	CAGCTAATTACCTTCTCTATCTACTCCAGAGAGACAGGAAGATCGACACC	412

```

RESULT 3
US-09-078-972A-18
: Sequence 18. Application US/09078972A
: Patent No. 6635806
:
: GENERAL INFORMATION:
: APPLICANT: KRIS, ALAN L.
: APPLICANT: LUEBHY, MICHAEL H.
: APPLICANT: VOYLES, DALE A.
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EXPRESSION OF TRANSGENES
: TITLE OF INVENTION: IN PLANTS
: FILE REFERENCE: DEKM:158
:
: CURRENT APPLICATION NUMBER: US/09/078,972A
: CURRENT FILING DATE: 1998-05-14
: NUMBER OF SEQ. ID NOS: 28
:
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ. ID NO 18
:
: LENGTH: 222
:
: TYPE: DNA
:
: ORGANISM: Artificial Sequence
:
: FEATURE:
:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
:
: US-09-078-972A-18

```

	Query Match	24.7%	Score 221;	DB 4;	Length 222;
	Best Local Similarity	100.0%	Pred. No.	5,8e-59;	
	Matches 221;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	674	CACTCGGCTTGCTACATTAAGTGAATGATGCATTAATTTTGGCAGAAGCCGTGAA	733		
Db	2	CACTCGGCTTGCTACATAAAGTGAATGATGATCATTAATTITGGCAAGAACCGTGA	61		
QY	734	AGCTACACAGCCGCGCTGACAGGACAAGAAACAAGAAACTGTGCTTAATGGAAGCTATA	793		
Db	62	AGCTACACAGCCGCGCTGACAGGACAAGAAACAAGAACTGTGCTTAATGGAAGCTATA	121		
QY	794	AATAACCCTAGTATGCTATGCACTTCTGCATCACCACTAACCCATATCTTCAGTCTATTT	853		
Db	122	AATAACCCTAGTATGCTATGCACTTCTGCATCACCACTAACCCATATCTTCAGTCTATTT	181		
QY	854	ACCTTCTCTATCTACTCCAGAGACACAGAAGATGCAACC	894		
Db	182	ACCTTCTCTATCTACTCCAGAGACACAGAAGATGCAACC	222		

RESULT 4
US-09-078-972A-22
; Sequence 22, Application US/09078972A
; Patent No. 6635806
; GENERAL INFORMATION:

APPLICANT: KRIS, ALAN L.
APPLICANT: LUEBHY, MICHAEL H.
APPLICANT: VOYLES, DALE A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EXPRESSION OF TRANSGENES
TITLE OF INVENTION: IN PLANTS
FILE REFERENCE: DEKM:158
CURRENT APPLICATION NUMBER: US/09/078,972A
CURRENT FILING DATE: 1998-05-14
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 2647
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-078-972A-22

Query Match 21.4%; Score 191.2; DB 4; Length 2647;
Best Local Similarity 68.9%; Pred. No. 4.5e-49;
Matches 524; Conservative 0; Mismatches 158; Indels 78; Gaps 16;

QY 143 TCTTTCAGAAATGTCGATTCCTGTTGGAGCATAGCAGTGTAGGTTCTCATTACCGGA 202
DB 534 TCTTTCGCGTCTTGGCAACATCTTGTGGAAGTACCAAGAGTTGCTC---CACGG 590
QY 203 TAACTCTGACAC---GTAAGTATGATGAGAAATCGAAGCAACCATTTGGATGAGCT 258
DB 591 TAACTCTGACACGATATGTAAGTATGATGAGAAATCGAAGCAACCATTTGGATGAGCT 649
QY 259 GTATGATTTGGTGTATTCATACAACTCGAAGCAACATACCAAAATTTGACGTCATG 318
DB 650 CTAT-AAATGGTGTATTCATACAA-ACGTGCGAAGATCAC-AAATTTGACGTCATG 706
QY 319 GATTGGTTCAGAAACAAATCGTCTCTGTTAGCTTTGATCAATGAAAGTATGATGATCAT 378
DB 707 GATTGGTTCAGAAACAAATCGTCTCTCGGT-----ACAAGAAAGTGTATGATCAT 756
QY 379 GAGTCACATGATCGATCTGTATATATATGCAATGATGTCACACGACAA-TTACAA 437
DB 757 GAGTCATGATGATGATAT-----ATACATGACACACGACATCACAACAAAG 806
QY 438 CAACCCATCTATACATCACAAGTTGTTTCTGAAAAACAAATATGATGATGATGATGAT 497
DB 807 TCAATCTACATTAAGAGTTAGTTTCACTTTCAAGTAAAAACAAAGTATGATGATGATGAT 865
QY 498 GGGCAATTAATCTGCTTGAACGCTAAGTAAATTTACAAAGCATATATCAACTATA 557
DB 866 AGGACATATATC---CTTGACGTGTAAAGTAAATTTACAAAGCATATATCAATTTATA 921
QY 558 TCTAATTAATAGTTCGTATATATATAGCAGATGATCATCAACACGTAACCTGTGAAA 617
DB 922 TCTAATTCGTTTATGATATATCACA-----ACCTGTAAAA 959
QY 618 GGCACAAATAGCCACGCAAAATGCAAAATTCATATGATGATGATGATGATGATGATGAT 677
DB 960 GGCACAAATAGCCACGCAAAATTTACAG-----TGAGTCAAAATTAACCT 1008
QY 678 CGGCTTCTCATATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 737
DB 1009 CACATGCTACATTAAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1068
QY 738 ACAACGCGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 797
DB 1069 ACA-----GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1123
QY 798 ACCCTAGTATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 855
DB 1124 ACCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1183
QY 856 CT-TCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 894

DB 1184 TTATATCTATCTACCGAGACAGACAAAGATCGACACC 1223

RESULT 5
US-09-078-972A-23

Sequence 23, Application US/09078972A

Patent No. 6635806

GENERAL INFORMATION:

APPLICANT: KRIS, ALAN L.

APPLICANT: LUEBHY, MICHAEL H.

APPLICANT: VOYLES, DALE A.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EXPRESSION OF TRANSGENES

TITLE OF INVENTION: IN PLANTS

FILE REFERENCE: DEKM:158

CURRENT APPLICATION NUMBER: US/09/078,972A

CURRENT FILING DATE: 1998-05-14

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 23

LENGTH: 3704

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-078-972A-23

Query Match 16.2%; Score 144.8; DB 4; Length 3704;
Best Local Similarity 64.2%; Pred. No. 1.7e-34;
Matches 443; Conservative 0; Mismatches 197; Indels 50; Gaps 13;

QY 214 CGTAAATGATGAGAAATACGGAACGAC---CATGGCATGTAGAGTGTATGATTTGG 269
DB 1914 CTTAAATGATGAGAAACAGAAACAAACATGCAATTTGCAATGATGATGATGATGATGATGAT 1973

QY 270 TGTATTCATACAACTCGCAGACATACCAAAATTTGACGTCATG-ATTGGTCA 328
DB 1974 TTGTATTCATACAACTCGCAGACATACCAAAATTTGACGTCATG-ATTGGTCA 2033

QY 329 GAAACAAATGATCTCTCTGTTAGCTTTGATCAATGATGATGATGATGATGATGATGATGAT 388
DB 2034 GAAACAAATGATCTCTCTCTGTTAGCTTTGATCAATGATGATGATGATGATGATGATGATGAT 2092

QY 389 GATTCGATCTGATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 448
DB 2093 ATACTCATCTGATATATGATG-CTTACAGCTCACAG---ACATTAACAAACATCTC---AT 2145

QY 449 TATCATCAACAAATGTTGTTTCAATGAAAAACAAATATGATGATGATGATGATGATGATGAT 508
DB 2146 ATGCAATTAACAAATGTTGTTTCAATGAAAAACAAATATGATGATGATGATGATGATGATGAT 2201

QY 509 CTTGCTTGAACGCTAAGTAAATTTACAAAGCATATATCAACTATATCTTAATTAATA 568
DB 2202 C-----CTTGACGATTAAGTAAATTTACAA-----CAAAAAAAGCCATATGTCAAGCTTA 2254

QY 569 AGTTCGTTATATATACGACGATGATGATCAACACCGTACCTGTGAAGGCAACAAAT 628
DB 2255 ATCTAATTCGTTTATGATGATCAACACCGTAC-----GAAAGCAACAAAT 2303

QY 629 GAGCAGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 688
DB 2304 GAGCAGCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2353

QY 689 ATAAAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 748
DB 2354 GTAAAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2413

QY 749 GTCAGTACACAGAAACAAAGAACTGTG---CTAATGAAGCTTAATTAATTAATTAATTAAT 804
DB 2414 CTGCGTGGCATTAGGAAACAAAGAAATGTTGTTAATTAATCAAGCTTAATTAATTAATTAAT 2473

QY 805 TATGCTATGATCTTCTCATACCACTACCAATATCTTCAAGTATTAATCTTCTCTAT 864

Db 2474 CATGCTGTGCACTTCTTCATCACCACCA-CTGGGCTTTCAGACCATTAGCTTATCTAC 2532
QY 865 CTACTCCAGAGACACAGAAAGATGACACC 894
Db 2533 TCCAGAGCGCAGAGAAACCCGATGACACC 2562

RESULT 6

US-09-621-976-2813/C
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813

Query Match 5.0%; Score 44.4; DB 4; Length 832;
Best Local Similarity 9.9%; Pred. No. 0.0019;
Matches 33; Conservative 160; Mismatches 141; Indels 0; Gaps 0;

QY 294 AACATCACAATAATTCAGCATGATGGTGTCAGAAAACAATCGTCTCTGTAGCTT 353
Db 342 WMMKKRRMYWYMMSTYACASRYRYTWGMMWMMKKMSTRMYCYWCKCMYRGRC 283
QY 354 GTACAAGAAGTGTGGTGTGATCATGATCAGTCCATCTGTATATATGCCAA 413
Db 282 AMYTMAGRWMSYAMGKRSMSMCTRMYYKGGSTYMWKCTCATWCYWKYWRM 223
QY 414 TAGCTCACGACGACAATTAACAACACCCATCTATATACCAAGTTGTTTCATG 473
Db 222 WSKTCWSSRGVYTSYSTSYMYWAMWYTCWMMGRWSTYMYAMGKWRVATT 163
QY 474 AAAAAACAATTAAGTATGACGAGAGGACAATAATCTCTTGAACGGTAAAGTAA 533
Db 162 WRRAMWMMWMAWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMWMMW 103
QY 534 TACAAGCATATATCAACCTATATCTAATTAATTAAGTCTTATATATACGACATGA 593
Db 102 WKTYSYWCWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCW 43
QY 594 TCATCAACAACCGTACTCTGTAAGGACAACAAA 627
Db 42 YWYWRAMKRRWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCWRCW 9

RESULT 7
US-08-232-463-14/C
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F.G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria

STATE: VA
COUNTRY: USA
ZIP: 22113-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232.463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935.313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpc-Fls

Query Match 4.8%; Score 42.6; DB 1; Length 7218;
Best Local Similarity 3.4%; Pred. No. 0.022;
Matches 12; Conservative 194; Mismatches 143; Indels 0; Gaps 0;

QY 450 ATATATCAACAAGTTGTTTCATGAAAAACAATAAGTATGACGAGGAGCAATATATC 509
Db 1455 AGAGATGAAGAAATTTGTACRCRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1396
QY 510 CTGCTGACGCGGAAGTGAATTACAAAGCATATATCAACCTATATCTAATTAATA 569
Db 1395 RRR 1336
QY 570 GTTGTTATATATGACGACGATGATCAACAACGTAACCTGTGAAGGACAACAAATG 629
Db 1335 RRR 1276
QY 630 AGCCACGCAAAAATGCAAGATGAATCCATATGATGACGAGAGTACACTCGGCTGTACA 689
Db 1275 RRR 1216
QY 690 TAAAGTGAATGATGATCAATTAATTTGGCAAGAACCGTGAAGCTACACACCGCTCG 749
Db 1215 RRR 1156
QY 750 TCAGTACACGACGACGACGAACTGTCTAATGCAAGCTAATAATA 798
Db 1155 RRR 1107

RESULT 8
US-09-621-976-8976
; Sequence 8976, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.


```

?
? FILE REFERENCE: GENSEP.054PR2
? CURRENT APPLICATION NUMBER: US/09/621,976
? CURRENT FILING DATE: 2000-07-21
? NUMBER OF SEQ ID NOS: 19335
? SOFTWARE: Patent.pm
? SEQ ID NO: 8976
? LENGTH: 399
? TYPE: DNA
? ORGANISM: Homo sapiens
US-09-621-976--8976

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Query Match	4.4%;	Score 39;	DB 4;	Length 359;
Best Local Similarity	10.7%;	Pred. No. 0.061;		
Matches 37;	Conservative 165;	Mismatches 140;	Indels 3;	Gaps 1;

Qy	474	AAAAACAAATTAAGTATCAGAGGGGCAATTAATCTGTGTGACGGTAAAGTAAT	533
Db	16	RAATRAYWGVTTTSSKTSKSRAKMSMKRRRRRAAMMMKSMCMKSKSKSWRSIGMMTK	75
Qy	534	TACAAAGCCATATATCAACTATATCTAATTAAATGATTGTTATATATACGACAGATGA	593
Db	76	RMKRGASAVSGYSYSMVTYMTRRMYRYRRKCACTKMPAAGMGAAGANMAIYAQMWTJA	135
Qy	594	TCATCAACAACCGTACCTGTGAAGAGCAACAAATGAGCCACGCAAAATGACAGATGAA	653
Db	136	WRRTAPMKYMAAMKSRSMRRRRRAYWAMYYMMARRTMGMASCTRGAYMASAGTYTMM	195
Qy	654	TCATATGATGACGAGCGTACCTCGGCTTGCTATATTAAGTAGTAGTCAATAAT	713
Db	196	YYMMRRKMYSAGMSMKMKWTRCASYSQMSYCMWGAQMMMYTTSFWSYSSYRC--	253
Qy	714	ATTGGCAAGAAACCGTGAAGACTACACAGCGCTGCTAGTAGACACAGAAACACAAGAA	773
Db	254	-TKTRSCCCSMSCWMTTYRRSWYCASCYYSYKTKRASCCMCCCMCKMRKMMAMMYMK	312
Qy	774	CTGTGCTATGGAAGCTATAATAACCTAGTAGTCCCTAGTCACT	818
Db	313	MTYCKTTSAMRYRSQYSAKWRRWMMCCAAVMMKCSMMWMCWT	357

```

RESULT 9
US-09-614-981-8/c
; Sequence 8, Application US/09614981
; Patent No. 6787687
; GENERAL INFORMATION:
; APPLICANT: GIOVANNONI, JAMES
; APPLICANT: TANKSLEY, STEVEN
; APPLICANT: PADMANABHAN, VEERARAGAVAN
; APPLICANT: RUEZINSKY, DIANE
; APPLICANT: VREBALOV, JULIA
; TITLE OF INVENTION: RIN GENE COMPOSITIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: TAMK:214
; CURRENT APPLICATION NUMBER: US/09/614,981
; CURRENT FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 13830
; TYPE: DNA
; ORGANISM: Tomato
; US-09-614-981-8

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Query Match	4.3%	Score 38.6;	DB 4;	Length 13830;
Best Local Similarity	47.3%;	Pred. No. 0.55;		
Matches 116;	Conservative 0;	Mismatches 129;	Indels 0;	Gaps 0;

Oy GTCTCCCTGTAGCTTGTCACATGAAGTATGTTGGTAGTATAGTCACTCATCGCATCTC 398
Db 5782 GTTTTTTTTTATTCTCCAAAGGATTCACTGGCGCTCAACTTGAAACAACATAAAAAGG 5722
Oy 399 GATATATATGCCAATAGCTCACAGACAACATTACAAAAAACCCCATCTACTTACATCAC 458

Db 5722 AAAATAGTAATAGTAAATTCAAAAATATAGTGTATCAATATGGCCATCTCTCTTGAC 5663
 Qy 459 AAAGTTGTTTCATGAAAAAACAAATTAAGTATGACAGAGGGGCAATATATCTTGCTTGA 518
 Db 5662 AATTAATATATTCACAAATTAATATATATATCCAAAGTGTTCGACGTAAAAACATCTCAAC 5603
 Qy 519 CGCGTAAGAAGATTTTCAAGCCATATCAACCTATCTATTAATAAGTTCGTTAT 578
 Db 5602 AATATTAAGTCTTAAAGTATGATATATATTAATTTCTCCATCTTAATTTTTTTAATTA 5543
 Qy 579 ATATA 583
 Db 5542 AAAATA 5538

```

RESULT 10
US-09-806-708B-22/c
; Sequence 22: Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAP1 promoters
US-09-806-708B-22

```

```

Query Match Similarity      4.3%; Score 38; DB 4; Length 1141;
Best Local Similarity      9.7%; Pred. No. 0.22;
Matches      76; Conservative 299; Mismatches 399; Indels 10; Gaps 2;

OY      113  TTCAAGGAGATACAGCGGCTCTTCTGACGTCTTTGACGAAATGTGGCATCTCTTGTTGAA 172
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      894  THGASHKRRTHHRTCRRTKYNNNNNNNARVYUYNHAAERMMMAWMTTRTNNNNNNNNN 835

OY      173  GCATAGCAGTGTAGTGTCTTCATTACGGAATATCTGACAGCGTAAGGTATGAGGATA 232
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      834  ACRRTTWMWBMKSWCNCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 775

OY      233  CGGAACGACCATGTGGCATGTGAGCTGTATGAAATGTGGTATATGACAAACAACCTGCA 292
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      774  NNYYHAAVTTTHDWCYKTYMNTYUWMDMTTMBTTRTNNNTTSNTMTNNNNNNNNMALTNN 715

OY      293  GAACATCAACAATATGACGCTCATGTGATGGTCAGAAACAATCGCTCTCTGTAGCT 352
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      714  NNNNNMKAYVAHANNNGCMWNNNDARTNNNTTYMRBRMNTNTKRYSTTRRHNYGAT 655

OY      353  TGTACAATGAAGTATGATGGTGAATCATATGATCAGTACAGTATCGATGTATATATGCCAA 412
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      654  NNNNNNNNNNNNNNNNSCTCTRMTMTBRWTKGGMIVRKVKVMDTTCYUVDVWMAASWV 595

OY      413  ATAGCTACAGCAACAACATTACAACAACAACCCATACATAC--ATGCAAGAAGTTDGT 469
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      594  WMYANMHCRCRVUTTRNNNTYCKSYAHSHYWTYSNNAMMYRXYSAANWSMABWTRNNWMM 535

OY      470  CATGAAAAAACAATAAGTATGACGAGGAGGACATATCTTGCTTTGACGCGCTAAAGTG 529
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      534  SGBVBMWAGTMMWRHNNNNNNNTDTRYYWMMKMBARBTYYVDSWCKNAKSMWGRGNBAMK 475

OY      530  AATTTCACAAAGCCATATATCACTATATCAATTAATTAAGTTGCTTATATACGACG 589
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Db 474 MWAANNADAGMDHTYMGNNNTMMRBAMKMMMAWCRBAYCCNNNNNNBACVHKKHM 415
Qy 590 ATATATATCAACAACCGTACCTGTGAAAGGCAACAAATAGCCACCCAAATATGCGAA 649
Db 414 RMTWKYMKAAACNNNNKAAKAYMRYAMMYSRDTTNTDMMMTSMBWMYTVDTYMRW 355
Qy 650 TGAATCATATGATGACGAAGTACACTCGGCTTGCTACATTAAGTAAGA-----T 702
Db 354 NNNNNNNNNRCKTTSMMMMMDHMTHTCTYGNNTWGSAYBMAAAMMAAGSNBVTYMCW 295
Qy 703 GACTCATTAATATTTGGCAAGAAACCGTGAAGCTACACAGCCGCTGCTAGTACACAGG 762
Db 294 RMTYMGKTMNTNNNNNNKAWYRTKTVAACNNRYYDDTAVMTBKRYKCYAYBYWYBYM 235
Qy 763 AACAACAAGAACTGTCTATCGAAGCTATAAATACCCCTAGTATGCTTATGCTCTC 822
Db 234 GKHHBWBWRABHRSNNMMWVCKNKYMSVHYAMRYBKWABAVGVGNMNMKRMAMHHW 175
Qy 823 CATCACCACTACCATATCTTCACTATATTAATTAATTAATTAATTAATTAATTAAT 882
Db 174 CATNN 115
Qy 883 AAGA 886
Db 114 KAKV 111

RESULT 11
US-09-791-211-10
; Sequence 10, Application US/09791211
; Patent No. 6448080
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Walt
; TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
; FILE REFERENCE: RTS-0205
; CURRENT APPLICATION NUMBER: US/09/791,211
; NUMBER OF SEQ ID NOS: 2001-02-23
; SEQ ID NO 10
; LENGTH: 98844
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 24962
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 64383
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 65468
; OTHER INFORMATION: unknown
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; LOCATION: 65469
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; LOCATION: 65471
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 87130
; OTHER INFORMATION: unknown
; NAME/KEY: unsure
; LOCATION: 89049
; OTHER INFORMATION: unknown
; OTHER INFORMATION: unknown
US-09-791-211-10

Query Match 4.3%; Score 38; DB 3; Length 98844;
Best Local Similarity 45.0%; Pred. No. 2.4;

Matches 143; Conservative 0; Mismatches 175; Indels 0; Gaps 0;
Qy 409 CCAATATGCTCACAGCAACATTTACAAACCCATATATATACATCAAAATTTGTT 468
Db 5131 CCTCATTTGAATCCACAAACAAATTCGMAATTTTCTGATATATCAAGAAACCATTTTC 5190
Qy 469 TCAATGAAAAAACAATTAAGTATCAGAGGGGCAATTAATCTTGTGACCGCTAAAGT 528
Db 5191 TTTAAGAAAAATTAATTAATATGTTTGAATATAAAGTTTCTGATATAAGTATATC 5250
Qy 529 GAATTTCAAAAGCATATATCAACTATATATTAATTAATTAATTAATTAATTAAT 588
Db 5251 CTGACTTTAATCATAGATCAAGATTAAGATATGATGATTTATACATATTTTGAATAGCAA 5310
Qy 589 GATGATATATCAACACCGTACCTGTGAAGCAACAAATAGAGCCAGCAAAATGCGAGA 648
Db 5311 AAAAAACAAATAGCTTTTTCCTCCAGTCTTACATTTGAGCACTCTTTTAATATCT 5370
Qy 649 ATGATATCATATATATGACGAAGCTACACTCGGCTTGCTACATTAAGTAAATGATGACTCA 708
Db 5371 ATTAACACTTTTCTATTAAGGACAAATTTTCCCTTCCCTAGGAAATGAAACCGAATAG 5430
Qy 709 TAAATATTTGGCAAGAAA 726
Db 5431 AAAAAATTTTGGCAAAAA 5448

RESULT 12
US-09-949-016-11760
; Sequence 11760, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PaacSeq for Windows Version 4.0
; SEQ ID NO 11760
; LENGTH: 161124
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11760

Query Match 4.2%; Score 37.6; DB 4; Length 161124;
Best Local Similarity 51.8%; Pred. No. 4.2;
Matches 85; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

Qy 615 AAAGCAACAAATGAGCCACGCAAAATGAGAAATGATATCATATGATGACGACGAC 674
Db 119833 AATCCCTTAATATTAATCACTTTCTCAATGCTTAAGAAACGTGATTAAGAAAAACATTA 119892
Qy 675 ACTCGGCTTGCTACATTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 734
Db 119893 AGTGGGTTTGTCAAAATATGAGAGTTTGATGAGAAAAAGTTTATTTAGTACTTGGCAA 119952
Qy 735 GCTACACAGCCGCTGCTAGTACGACAGGAAACAAAGAACTGTG 778
Db 119953 TGTTGTATCCACTGTGTTTAGCCACATCACAAAGAACCTGGG 119996

RESULT 13
US-09-949-016-14178
; Sequence 14178, Application US/09949016
; Patent No. 6812339

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Db      61  TATAGCAGCAGAAATCACTGTCTTGTCTACAGACAGAACCAATGCATCAACTTCAAGGG 120
Qy      121  AGTACCGCGCTCTTCTTGACTGTCTTTCAGAAATGTGCGACTTCTTGTGGAGCATGCA 180
Db      121  AGTACCGCGCTCTTCTTGACTGTCTTTCAGAAATGTGCGACTTCTTGTGGAGCATGCA 180
Qy      181  GTGTAGGTTGCTCATTCACGGATATATCTGCACAGCTAAAGTATGAGAAATACGGAACGA 240
Db      181  GTGTAGGTTGCTCATTCACGGATATATCTGCACAGCTAAAGTATGAGAAATACGGAACGA 240
Qy      241  CCATTGGCATGTAGAGCTGTATGTAATGGTGTATTCATACAACTCCGAGAACATCA 300
Db      241  CCATTGGCATGTAGAGCTGTATGTAATGGTGTATTCATACAACTCCGAGAACATCA 300
Qy      301  CAAAATTGCAACGTCAATGGAATGGGTGTCAGAAACAAATCGTCTCTTGTAGCTTGTACAA 360
Db      301  CAAAATTGCAACGTCAATGGAATGGGTGTCAGAAACAAATCGTCTCTTGTAGCTTGTACAA 360
Qy      361  GAAGTGTGTTGATCATGAGTCACTGATCCGATCGATATATATATGCGCAATAGCTCA 420
Db      361  GAAGTGTGTTGATCATGAGTCACTGATCCGATCGATATATATATGCGCAATAGCTCA 420
Qy      421  CACGACAACTTACAAACCAACCCCATCTATACATCAAAAGTTTGTTCATGAAAAAC 480
Db      421  CACGACAACTTACAAACCAACCCCATCTATACATCAAAAGTTTGTTCATGAAAAAC 480
Qy      481  AAATAGTATGCAAGAGGGAACAATAATCTCTGCTTACCGGTAAAGTGAATTTTACAAG 540
Db      481  AAATAGTATGCAAGAGGGAACAATAATCTCTGCTTACCGGTAAAGTGAATTTTACAAG 540
Qy      541  CCATATATCAACCTATATCTAATTAATAGTTCGTATATATATATATATATATATATATAT 600
Db      541  CCATATATCAACCTATATCTAATTAATAGTTCGTATATATATATATATATATATATATAT 600
Qy      601  CAACCGTACCTGTGAAAGGCAACAAATGAGCCACGCAAAATGCAAGATGCATAT 660
Db      601  CAACCGTACCTGTGAAAGGCAACAAATGAGCCACGCAAAATGCAAGATGCATAT 660
Qy      661  GATGACGAAGCTACACTCGGCTTGTCTATTAAGTGAATGATGATCAATAATTTTGGC 720
Db      661  GATGACGAAGCTACACTCGGCTTGTCTATTAAGTGAATGATGATGATCAATAATTTTGGC 720
Qy      721  AAGAAACCGTGAAGAGCTACACAGCGCTGCTAGTAGCAGAGAACACAAAGAACTGTGCT 780
Db      721  AAGAAACCGTGAAGAGCTACACAGCGCTGCTAGTAGCAGAGAACACAAAGAACTGTGCT 780
Qy      781  AATGGAAGCTATAAATAAACCCTAGTATGCTATGCACTTCTCATCAACCACTACCATAT 840
Db      781  AATGGAAGCTATAAATAAACCCTAGTATGCTATGCACTTCTCATCAACCACTACCATAT 840
Qy      841  CTTGAGCTATTTTACCTTCTCTATCTACTCCAGAGACACAGAAATGCACACC 894
Db      841  CTTGAGCTATTTTACCTTCTCTATCTACTCCAGAGACACAGAAATGCACACC 894

RESULT 2
AR411335 894 bp DNA linear PAT 18-DEC-2003
LOCUS     AR411335
DEFINITION Sequence 8 from patent US 6635806.
ACCESSION AR411335
VERSION   AR411335.1 GI:40163439
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 894)
AUTHORS  Kriz, A.L., Luethy, M.H. and Voyles, D.A.
TITLE     Methods and compositions for expression of transgenes in plants
JOURNAL   Patent: US 6635806-A 8 21-Oct-2003;
FEATURES  Location/Qualifiers
           1..894
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ORIGIN
/mol_type="genomic DNA"
Query Match 100.0%; Score 894; DB 6; Length 894;
Best Local Similarity 100.0%; Pred. No. 1,4e-217;
Matches 894; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1  GGAACGGTTACACACACCACTGTGGGTGCTTCAAGGCGAGTACCAAACTATAGCATCA 60
Db      1  GGAACGGTTACACACACCACTGTGGGTGCTTCAAGGCGAGTACCAAACTATAGCATCA 60
Qy      61  TATAGCAGCAGAAATCACTGTCTTGTCTACAGACAGAACCAATGCATCAACTTCAAGGG 120
Db      61  TATAGCAGCAGAAATCACTGTCTTGTCTACAGACAGAACCAATGCATCAACTTCAAGGG 120
Qy      121  AGTACCGCGCTCTTCTTGACTGTCTTTCAGAAATGTGCGACTTCTTGTGGAGCATGCA 180
Db      121  AGTACCGCGCTCTTCTTGACTGTCTTTCAGAAATGTGCGACTTCTTGTGGAGCATGCA 180
Qy      181  GTGTAGGTTGCTCATTCACGGATATATCTGCACAGCTAAAGTATGAGAAATACGGAACGA 240
Db      181  GTGTAGGTTGCTCATTCACGGATATATCTGCACAGCTAAAGTATGAGAAATACGGAACGA 240
Qy      241  CCATTGGCATGTAGAGCTGTATGTAATGGTGTATTCATACAACTCCGAGAACATCA 300
Db      241  CCATTGGCATGTAGAGCTGTATGTAATGGTGTATTCATACAACTCCGAGAACATCA 300
Qy      301  CAAAATTGCAACGTCAATGGAATGGGTGTCAGAAACAAATCGTCTCTTGTAGCTTGTACAA 360
Db      301  CAAAATTGCAACGTCAATGGAATGGGTGTCAGAAACAAATCGTCTCTTGTAGCTTGTACAA 360
Qy      361  GAAGTGTGTTGATCATGAGTCACTGATCCGATCGATATATATATATATATATATATATAT 420
Db      361  GAAGTGTGTTGATCATGAGTCACTGATCCGATCGATATATATATATATATATATATATAT 420
Qy      421  CACGACAACTTACAAACCAACCCCATCTATACATCAAAAGTTTGTTCATGAAAAAC 480
Db      421  CACGACAACTTACAAACCAACCCCATCTATACATCAAAAGTTTGTTCATGAAAAAC 480
Qy      481  AAATAGTATGCAAGAGGGAACAATAATCTCTGCTTACCGGTAAAGTGAATTTTACAAG 540
Db      481  AAATAGTATGCAAGAGGGAACAATAATCTCTGCTTACCGGTAAAGTGAATTTTACAAG 540
Qy      541  CCATATATCAACCTATATCTAATTAATAGTTCGTATATATATATATATATATATATATAT 600
Db      541  CCATATATCAACCTATATCTAATTAATAGTTCGTATATATATATATATATATATATATAT 600
Qy      601  CAACCGTACCTGTGAAAGGCAACAAATGAGCCACGCAAAATGCAAGATGCATAT 660
Db      601  CAACCGTACCTGTGAAAGGCAACAAATGAGCCACGCAAAATGCAAGATGCATAT 660
Qy      661  GATGACGAAGCTACACTCGGCTTGTCTATTAAGTGAATGATGATCAATAATTTTGGC 720
Db      661  GATGACGAAGCTACACTCGGCTTGTCTATTAAGTGAATGATGATGATCAATAATTTTGGC 720
Qy      721  AAGAAACCGTGAAGAGCTACACAGCGCTGCTAGTAGCAGAGAACACAAAGAACTGTGCT 780
Db      721  AAGAAACCGTGAAGAGCTACACAGCGCTGCTAGTAGCAGAGAACACAAAGAACTGTGCT 780
Qy      781  AATGGAAGCTATAAATAAACCCTAGTATGCTATGCACTTCTCATCAACCACTACCATAT 840
Db      781  AATGGAAGCTATAAATAAACCCTAGTATGCTATGCACTTCTCATCAACCACTACCATAT 840
Qy      841  CTTGAGCTATTTTACCTTCTCTATCTACTCCAGAGACACAGAAATGCACACC 894
Db      841  CTTGAGCTATTTTACCTTCTCTATCTACTCCAGAGACACAGAAATGCACACC 894

RESULT 3
BD226670 412 bp DNA linear PAT 17-JUL-2003
LOCUS     BD226670
DEFINITION Methods and compositions for expression of transgenes in plants.
ACCESSION BD226670
```

VERSION	BD226670.1	GI:33036440
KEYWORDS	JP 2002533057-A/19.	
SOURCE	synthetic construct	
ORGANISM	synthetic construct	
REFERENCE	other sequences; artificial sequences.	
AUTHORS	1 (bases 1 to 412)	
TITLE	Kriz, A.L., Luethy, M.H. and Voyles, D.A.	
JOURNAL	Method and compositions for expression of transgenes in plants	
COMMENT	Patent: JP 2002533057-A 19 08-Oct-2002;	
	DERALB GENETICS CORP	
	OS Artificial Sequence	
	PN JP 2002533057-A/19	
	PD 08-OCT-2002	
	PP 14-MAY-1999 JP 2000548450	
	PR 14-MAY-1998 US 09/078972	
	PI ALAN L KRIZ, MICHAEL H LUETHY, DALE A VOYLES	
	PC A01H1/00, C12N5/10, C12N15/09, C12N5/00, C12N15/00 CC	
	Description of Artificial Sequence: Synthetic Primer FH	Key
	Location/Qualifiers	
FT	1..412	
source	Location/Qualifiers	
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	/mol_type="genomic DNA"	
	/db_xref="taxon:32630"	
ORIGIN		
Query Match	46.0%; Score 411; DB 6; Length 412;	
Best Local Similarity	100.0%; Pred. No. 3.8e-94;	
Matches	411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	484 TAAATGATCAGAGAGGGAACAATAATCTTGGCTTGAACGGTAAGTAATTACAAAGCA 543	
DB	2 TAAATGATCAGAGAGGGAACAATAATCTTGGCTTGAACGGTAAGTAATTACAAAGCA 61	
QY	544 TATATCAACCTATATCTTAATTAATTAAGTTCGTTATATATATACGCAGATGATCATCAAA 603	
DB	62 TATATCAACCTATATCTTAATTAATTAAGTTCGTTATATATATACGCAGATGATCATCAAA 121	
QY	604 CCGTACCTGTGAAGGCAACAATAATGAGCCACGCAAAATGCGAATGATCATCATATGAT 663	
DB	122 CCGTACCTGTGAAGGCAACAATAATGAGCCACGCAAAATGCGAATGATCATCATATGAT 181	
QY	664 GACGAACTGACACTCGCGCTTGTCTACATTAAGTGAATGATGATCATTAATATTTGGCAAG 723	
DB	182 GACGAACTGACACTCGCGCTTGTCTACATTAAGTGAATGATGATCATTAATATTTGGCAAG 241	
QY	724 AAACCGTGAAGCTTACACAGCCGTCGTGATGACACAGAAACACAAAGAACTGTGCTAAT 783	
DB	242 AAACCGTGAAGCTTACACAGCCGTCGTGATGACACAGAAACACAAAGAACTGTGCTAAT 301	
QY	784 CGAAGCTTAATAATACCCCTAGATGCGCATGACCTTCCATACCACTACCCATATCTT 843	
DB	302 CGAAGCTTAATAATACCCCTAGATGCGCATGACCTTCCATACCACTACCCATATCTT 361	
QY	844 CAGTCTATTTACTTCTCTATCTACTCCAGAGAGACAGAAAGATGACACC 894	
DB	362 CAGTCTATTTACTTCTCTATCTACTCCAGAGAGACAGAAAGATGACACC 412	
RESULT 4		
AR411346	412 bp	DNA
LOCUS	Sequence 19 from patent US 6658906.	linear
DEFINITION		PAT 18-DEC-2003
ACCESSION	AR411346	
VERSION	AR411346.1	GI:40163450
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	1 (bases 1 to 412)	
AUTHORS	Kriz, A.L., Luethy, M.H. and Voyles, D.A.	

FEATURES	JOURNAL	PATENT
TITLE	Methods and compositions for expression of transgenes in plants	
JOURNAL	US 6635806-A 19 21-OCT-2003;	
FEATURES	Location/Qualifiers	
source	1..412	/organism="unknown"
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Best Local Similarity	100.0%; Pred. No. 3,8e-94;	
Matches	411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	484 TAACTATGACGAGGGGACAATAATCTTGTGCTTGACCCGTTAAGTGAATTTCACAAAGCA	543
DB	2 TAACTATGACGAGGGGACAATAATCTTGTGCTTGACCGTTAAGTGAATTTCACAAAGCA	61
OY	544 TATATCAACCATAATCTTAATTAATAGTGGTATATATACGCAGATGATCATCACAA	603
DB	62 TATATCAACCATAATCTTAATTAATAGTGGTATATATACGCAGATGATCATCACAA	121
OY	604 CCGTAGCTGTGAAAAGGCAAAAAATGACCAACGCAAAAAATGACAGAATGAAATCCATATGAT	663
DB	122 CCGTAGCTGTGAAAAGGCAAAAAATGACCAACGCAAAAAATGACAGAATGAAATCCATATGAT	181
OY	664 GACGACAGTACACTCGGCTTGCTATCAATAAGTAAATGATATGATCATTAATTTTGGCAG	723
DB	182 GACGACAGTACACTCGGCTTGCTATCAATAAGTAAATGATATGATCATTAATTTTGGCAG	241
OY	724 AAACCGTGAAGACATCACAGCCGTCGTCAGTACAGACAGAAACAAAGAACTGTGCTAAT	783
DB	242 AAACCGTGAAGACATCACAGCCGTCGTCAGTACAGACAGAAACAAAGAACTGTGCTAAT	301
OY	784 CGAAGCATTAATAATTAACCTAGTATGCCATATGCACTTCCATCAGCACTAACCCATATCTT	843
DB	302 CGAAGCATTAATAATTAACCTAGTATGCCATATGCACTTCCATCAGCACTAACCCATATCTT	361
OY	844 CAGTCTATTATTCCTTCTCTATCTACTCAAGACGACAGAAAGATGCACCC	894
DB	362 CAGTCTATTATTCCTTCTCTATCTACTCAAGACGACAGAAAGATGCACCC	412
RESULT 5		
LOCUS	BD226669	222 bp DNA linear PAT 17-JUN-2003
DEFINITION	Methods and compositions for expression of transgenes in plants.	
ACCESSION	BD226669	
VERSION	BD226669.1 GI:33036439	
KEYWORDS	JP 2002533057-A/18.	
SOURCE	Synthetic construct	
ORGANISM	Synthetic construct	
REFERENCE	other sequences; artificial sequences.	
AUTHORS	1 (bases 1 to 222)	
TITLE	Kriz,A.L., Luethy,M.H. and Voyles,D.A.	
JOURNAL	Methods and compositions for expression of transgenes in plants	
COMMENT	Patent: JP 2002533057-A 18 08-OCT-2002;	
	DEKALB GENETICS CORP	
	OS Artificial Sequence	
	PN JP 2002533057-A/18	
	PD 08-OCT-2002	
	PF 14-MAY-1999 JP 2000548450	
	PR 14-MAY-1998 US 09/078972	
	PI ALAN L KRIZ, MICHAEL H LUETHY, DALE A VOYLES	
	PC AO1H1/00,C12N5/10,C12N15/09,C12N5/00,C12N15/00 CC	
	Description of Artificial Sequence: Synthetic Primer FH	
	Location/Qualifiers	Key
FT	1..222	
FT	source	
FEATURES	location/Qualifiers	
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Db 1124 ACCCTGCTAGCCCTATGACATCTCCATCCACCACCTGCTCTTCAATTCAGCCTATTAAAC 1183

Qy 856 CT-TCTCTATCTACTCCAGAGACAGACAAGATGACACC 894

Db 1184 TTATATCTATCTACTCCAGAGACAGACAAGATGACACC 1223

RESULT 8
AR411349
LOCUS
DEFINITION Sequence 22 from patent US 6635806.
ACCESSION AR411349
VERSION AR411349.1 GI:40163453
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2647)
AUTHORS Kriz,A.L., Luethy,M.H. and Voyles,D.A.
TITLE Methods and compositions for expression of transgenes in plants
JOURNAL Patent: US 6635806-A 22 21-OCT-2003;
FEATURES
Source 1..2647
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/mol_type="genomic DNA"

ORIGIN

Query Match 21.4%; Score 191.2; DB 6; Length 2647;
Best Local Similarity 68.9%; Pred. No. 4,7e-38;
Matches 524; Conservative 0; Mismatches 158; Indels 78; Gaps 16;

Qy 143 TCTTTGGAATTGTCGATCTTGTGGAGCATAGCAGTGTAGTGTCTTATTCAGCA 202

Db 534 TCTTCCGGTCTTGGCAATCTTGTGGAGATACCAAGAGTTGCTC--CAGCGG 590

Qy 203 TAACTTCGACAC--GTAAAGTATGAGAAATACGAAACGACCATTTGGCATGTAGAGT 258

Db 591 TAACTTCGACACGATGTAAAGTATGAGAAATGAGCAATTTGCGCATGTAA-AGCT 649

Qy 259 GTATGAATTTGGTGTATTCATCAACAACCTGCGAAACATCAAAAATTTGACGTCATG 318

Db 650 CTAT-ATTGGTGTATTCATCAACA-ACGTGCGAAACATCAC-AAATTGACGTCGAAG 706

Qy 319 GATTGGTCGAAACAATGCTCTCTGTAGCTTTGACATGAAGTATGATGTAGTCAT 378

Db 707 GATTGGTCGAAACAATGCTCTCTGTAGCTTTGACATGAAGTATGATGTAGTCAT 756

Qy 379 GAGTCACATGATCGATCTGATATATATGCAATATAGTCACAGCAACA-TTACAAA 437

Db 757 GAGCATGTGATCTGATAT-----ATACATAGCACACGACATCAACAAACAG 806

Qy 438 CAACCCATATCTATATCAACAAGTTTTCATGAAAAACAATAATATATGATGACAG 497

Db 807 TCATATCACTTACAGAGTATGTTTCACTTCAAGTAAAAACAAGTAGGCCGGA-GAG 865

Qy 498 GGGACATATCTCTGCTTGAACGCTTAAAGTATTTACAAAGCCATATATCAACCTATA 557

Db 866 AGGACATATATC---CTTGAACGCTTAAAGTATTTACAAAGCCATATATCAACCTATA 921

Qy 558 TCTAATTAATTAAGTCTGTTATATATATATATGACAGATGATCATCAACAACGTCGTGAAA 617

Db 922 TCTAATTCGTTTCACTGATATATCAACA-----ACCTGTAAAA 959

Qy 618 GGGACAAAATGACCCAGCAAAAATGACAGATGATCATATGATGACGAACGTACACT 677

Db 960 GGGACAAAATGACCCAGCAAAAATTAAG-----TGAGTCCAAATAAACCT 1008

Qy 678 CGGCTTCTATATTAAGTATGATGATTAATATTTGGCAAGAACGCTGAAAGCT 737

Db 1009 CACATGCTATCAATAAAGTATGATGATGATCTGATATCTGGCAAGAAACGTGAAAGCT 1068

Qy 738 ACACAGCCGTGCTAGTAGCACAGAAACAACAAGAACTGTGATGAAAGCTTAAATA 797

Db 1069 ACA-----GTCAATGCTAGCAAAAGAAACAGAAAGAAATGCTATTAAGCTATTAAATA 1123

Qy 798 ACCCTAGTATGCTATGACATCTTCCATTCACCAATACCATAT--CTTCACTATTATAC 855

Db 1124 ACCCTGCTAGCCCTATGACATCTCCATCCACCACCTGCTCTTCAATTCAGCCTATTAAAC 1183

Qy 856 CT-TCTCTATCTACTCCAGAGACAGACAAGATGACACC 894

Db 1184 TTATATCTATCTACTCCAGAGACAGACAAGATGACACC 1223

RESULT 9
SVKAF
LOCUS
DEFINITION S. vulgare gene for gamma-kafirin.
ACCESSION X62480
VERSION X62480.1 GI:671655
KEYWORDS gamma-kafirin; gamma-prolamin; seed storage protein.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 2647)
AUTHORS de Freitas,F.A., Yunes,J.A., da Silva,M.J., Arruda,P. and Leite,A.
TITLE Structural characterization and promoter activity analysis of the gamma-kafirin gene from sorghum
JOURNAL Mol. Gen. Genet. 245 (2), 177-186 (1994)
MEDLINE 95115665
PUBMED 7816025
REFERENCE 2 (bases 1 to 2647)
AUTHORS Leite,A.
TITLE Direct Submission
JOURNAL Submitted (07-OCT-1991) A. Leite, Centro de Biologia Molecular e, Engenharia Genetica, Universidade Estadual de Campinas, Cidade Universitaria 'Zeferino Vas', Cep 13.081-Campinas-Sao Paulo, BRAZIL
FEATURES
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/note="putative"

ORIGIN

Query Match 21.4%; Score 191.2; DB 8; Length 2647;
Best Local Similarity 68.9%; Pred. No. 4,7e-38;
Matches 524; Conservative 0; Mismatches 158; Indels 78; Gaps 16;

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Db 534 TCTTGCGGTGCTTGCGAACAATCTTGTTGGAGATACAGAAAGTTGCTC---CAGGG 590
Qy 203 TAATCTCGAACAC---GTAAGTATAGAGAAATACGAAACGACATTTGGATGAGAGCT 258
Db 591 TAATCTTGACACGTATGTAAGATGATAGGAAACATTTGAAACGAAATTTGGATGTA-AGCT 649
Qy 259 GTATGAATTTGGTGTATTCATACAAACAAGCTGCGAAGACATCAAAAATTTGACCTCATG 318
Db 650 CTAT-AATTTGGTGTATTCATACAA-ACGTGCGAAGACATCAC-AAATTTGACCTCAAG 706
Qy 319 GATTGGGTCAAAAACAATCGTCTCTTTGAGTTGATCAATGAAGTGTGATCAT 378
Db 707 GATTGGGTCAAAAACAATCGTCTCTCTGT-----ACAACGAAGTGTGATCAT 756
Qy 379 GAGTCACATGATCCGATCTGATATATATGCCAAATAGCTCACACGACAA-TTACAA 437
Db 757 GAGCAATGTTGATCTGATAT-----ATACATGACACACGACATCACAAACAG 806
Qy 438 CAACCCCATCTATACATCAACAAGTTGTTTCATGAAAAACAATTAATGATGACAGAG 497
Db 807 TCATACATCAATACAGAGTTAGTTTCACTTCAAGTAAACAAAGTAGGCGGGA-GAG 865
Qy 498 GGGCAATTAATCTTGGCTTGAACGGTAAGTGAATTTACAAAGCCATATATCAACTATA 557
Db 866 AGGCAATTAATC---CTTGACGTGTAAGTGAATTTACAAAGCCATATATCAATTTATA 921
Qy 558 TCTTAATTAATGATCTGTTATATATAGCAGATGATCATCAACCCGATCTCTGAAA 617
Db 922 TCTTAATCTGTTCAATGATATCAACA-----ACGTGTAAGA 959
Qy 618 GGGCAAAAATGAGCCACGCAAAAATGCAATGATCATGATGACGACATCAACT 677
Db 960 GGGCAAAAATGAGCCACGCAAAAATTTACAG-----TGAGTCCAAATTAACCT 1008
Qy 678 CGGCTGCTCAATTAAGTGAATGATGATCAATTAATTTGGCAAGAACCGTGAAGCT 737
Db 1009 CACATGCTACATTAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 1068
Qy 738 ACACAGCCGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 797
Db 1069 ACA-----GTCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1123
Qy 798 ACCCTAGTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 855
Db 1124 ACCCTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1183
Qy 856 CT-TCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 894
Db 1184 TTATATCTATCTACTCCAGAGCAGACAAAGATCGACACC 1223

RESULT 10
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LOCUS BD226674
DEFINITION Methods and compositions for expression of transgenes in plants.
ACCESSION BD226674.1 GI:33036444
VERSION UP 2002533057-A/23.
KEYWORDS UP 2002533057-A/23.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1. (bases 1 to 3704)
AUTHORS Kitz,A.L., Luethy,M.H. and Voyles,D.A.
TITLE Methods and compositions for expression of transgenes in plants
JOURNAL Patent: JP 2002533057-A 23 08-OCT-2002;
DEKALB GENETICS CORP
OS Artificial Sequence
PN JP 2002533057-A/23
PD 08-OCT-2002
PF 14-MAY-1999 JP 2000548450
PR 14-MAY-1998 US 09/078972
PI ALAN L. KRIZ, MICHAEL H. LUTHEY, DALE A. VOYLES
PC A01H1/00, C12N5/10, C12N15/09, C12N5/00, C12N15/00 CC

DESCRIPTION OF ARTIFICIAL SEQUENCE: Synthetic Primer FH Key
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Location/Qualifiers
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ORIGIN
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Best Local Similarity 64.2%; Pred. No. 3.3e-26;
Matches 443; Conservative 0; Mismatches 197; Indels 50; Gaps 13;
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Db 1914 CTTAAGTATGAGGATAGGAAACGACATGATGATGATGATGATGATGATGATGATG 1973
Qy 270 TGTATGCTATACAAACCTGCAAGACATCAACAAATTTGACGCTAATGG-ATTGGTCA 328
Db 1974 TGTATGCTATACAAACCTGCAAGACATCAACAAATTTGACGCTAATGGTATTGGTAA 2033
Qy 329 GAAACAAATGCTCTCTGAGCTTGTATGATGATGATGATGATGATGATGATGATGATG 388
Db 2034 GAAACAAATGCTCTCTGAGCTTGTATGATGATGATGATGATGATGATGATGATGATG 2092
Qy 389 GATTCATCTGATATATATGCAATAGCTCACGCAACATTTACAAACCAACCTATC 448
Db 2093 ATACTCATCTGATATATATGATGATGATGATGATGATGATGATGATGATGATGATG 2145
Qy 449 TATACATCAACAAATGTTGTTGATGAAACAAATTAATGATGAGGAGGACATTAAT 508
Db 2146 ATTCATTTACAAAGATGTTTCTATGAAAAATTAATA---TAGCCGACAGGACAAAT 2201
Qy 509 CTTGCTTGAACGCTAAGTGAATTTACAAAGCCATATCACTATATCTTAATTAATA 568
Db 2202 C---CTTGAAGTGAATTAATTTACAA---CAAAAAAAGCCATATGTCMAAGCTAA 2254
Qy 569 AGTTGCTTATATATGAGCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 628
Db 2255 ATCTAATCTGTTTATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2303
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Db 2354 GTAAAGAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2413
Qy 749 GTCAGTACACAGAAACAAAGAACTGTG---CTAATGAGCTTAATTAACCTTAG 804
Db 2414 CTGCTGTCATAGGAAACAAAGAAATGTTAATTAATTAATTAATTAATTAATTAATTA 2473
Qy 805 TATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 864
Db 2474 CATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2532
Qy 865 CTACTCCAGAGACAGAAAGATGACACC 894
Db 2533 TCCAGAGGCGAAGAAACCGATGACACC 2562

RESULT 11
AR411350 3704 bp DNA linear PAT 18-DEC-2003
LOCUS AR411350
DEFINITION Sequence 23 from patent US 6635806.
ACCESSION AR411350
VERSION AR411350.1 GI:40163454
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

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OY		805	TATGCCCATATGACTTCTCCATCACCACTACCACATATCTTGAGCTCATTATTA	CCT	864
D6		2474	CATCCCTGTGACAATTCTTCATCACCACCA-CTGGGTCITTCAGACCAATTAGCTTATCTAC		2532
OY		865	CTACTCCAGAGACACAGAAGATGCACGC		894
D6		2533	TTCCAGAGCGCAGGAAGAACCCGATGACACC		2562
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Locus	S78780	1889 bp	mRNA	linear	PLN 06-MAY-2003
DEFINITION	(ggmma-zelina)-opaque2 modifier [S' region] [Zea mays=maize, Tuxpeno				
ACTION	CMS 450, mRNA Partial, 1889 nt].				
VERSION	S78780				
KEYWORDS	S78780..1 GI.1037129				
SOURCE	Zea mays				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD				
REFERENCE	clade; Panicoidae; Andropogoneae; Zea.				
AUTHORS	1 (bases 1 to 1889)				
	Lopes,M.A., Takasaki,K., Boswick,D.E., Helencjars,T. and				
	Larkin,B.A.				
TITLE	Identification of two opaque2 modifier loci in quality protein				
JOURNAL	maize				
MEDLINE	Mol. Gen. Genet. 247 (5) , 603-613 (1995)				
PUBMED	95327057				
REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI gi 569169058] from the original journal article.				
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	Best Local Similarity	64.1%; Pred. No. 8; 9e-26;			
	Matches 442; Conservative	0; Mismatches 198; Indels 50; Gaps 13;			
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OY	270	TGTATTCATACMACAACTCGCAGAAATCATCAAATTTGCAGTCGAATGG-A TTGGGTCA			328
D6	539	TTGTATCCTTAACAACATCAAGAAACATCAACCAAAATTGCAAGTCAAGGATATTGGTAA			598
OY	329	GAAAACAAATCGCTCTCTGTAGCTTGTACAAAGAAATGATAGTGAATGATACACT			388
D6	599	GAAACAAATCAACAAATCCTCTCTGTGTGGCAAAGAAACGCTGAGTATG-CGAGATC			657
OY	389	GATCGATCTGATATATATATGCCAAATAGCTCACAGACAACTTCAACAAACCCCATTAC			448

Db	658	ATATCATCTCGATATATCATG-CTTTAGAGCTCACAG-ACATTACAAAACACTC--AT	710
Oy	449	TATATCATCACAAAGTTTGTTCATGAAAAAAACAATAGTATGACAGAGGGACATTAAT	508
Db	711	ATTGCATTACAAAAGATCGTTTCATGAAAAATTA--TAGGCCGACAGCAAAAAT	766
Oy	509	CCTTGCTTGAAGCGTAAAGTGAATTTATCAAAAGCCATATCAACTATATCTTAATTATA	568
Db	767	C-----CTTGAACGTGTAAAGTAAATTTACAA--CAAAAAAAGCCATATGTCAAGCTAA	819
Oy	569	AGTTCGTTATATATAGCGACGATGATCATCAACAACGTAACCTGTCTGTAAAGCAACAAAT	628
Db	820	ATCTAATTCGTTTTTACCTAGATCAACAACCTGTA-----GAAGCCAACAAACT	868
Oy	629	GAGCCATGCAAAAAATGAGATGATTCATATGATGACGAACGTACACTCGACTTGGCTAC	688
Db	869	GAGCAGCGCAAGATACAGAAATGATTTCCAAATGA-----ACATGACGTGTACT	918
Oy	689	ATAAAGTAATGATGACTCATTAATATTTGGCAGAAACCGTGAAAGCTACACAGCCGTC	748
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Oy	749	GTCAGTAGCACAGGAACAAGAAGCTGTG-----CTAATGGAAGCTTAATAATACCTAG	804
Db	979	CTCGGTGCAATACAAACAAGAATATGTGTTAATTAATCAAAAGCTATTAATTAACGCTGC	1038
Oy	805	TATGCTCATGACACTTTCATATCAGCACTACCCATATCTTGACTATTTTACCTTCTGTAT	864
Db	1039	CATGCTGTGTGACTTTCCTCATCACCAACA--CTGGGCTTTCAGACCACTTACTTATCTTAC	1097
Oy	865	CTACTCCAGAGACACAGAAAGATGCAAC	894
Db	1098	TTCAAGACGCAAGAAACCGATGCAACC	1127

RESULT 14				
LOCUS				
ZM27KZ2NB	ZM27KZ2NB	3695 bp	DNA	linear
DEFINITION	Z. mays 27kDa zein locus DNA.			
ACCESSION	X56118			
VERSION	X56118.1	GI:22100		
KEYWORDS	zein protein.			
SOURCE	Zea mays			
ORGANISM	Zea mays			
REFERENCE	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.			
AUTHORS	1 (bases 1 to 3695)			
TITLE	Dae,O.P., Ward,K., Ray,S. and Messing,J.			
JOURNAL	Sequence variation between alleles reveals two types of copy correction at the 27-kDa zein locus of maize			
MEDLINE	Genomics 11 (4), 849-856 (1991)			
PUBMED	1783393			
REFERENCE	2 (bases 1 to 3695)			
AUTHORS	Messing,J.			
TITLE	Direct Submission			
JOURNAL	Submitted (24-SEP-1990) J. Messing, Rutgers State University, WAKESMAN INSTITUTE, HOES LANE, PISCATAWAY NEW JERSEY 08855, USA			
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TATA_signal	2448..2451			
misc_feature	2482..2484			
	/standard_name="Cap Site"			
ORIGIN				

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 24, 2005, 06:10:33 ; Search time 541 Seconds
(without alignments)
9782.345 Million cell updates/sec

Title: US-10-660-097-8

Perfect score: 894
Sequence: 1 ggacgcgttaccagacacca.....ggacacagaatcgcacacc 894

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	894	100.0	894	AAZ45473	AAZ45473 Nucleotide
2	411	46.0	412	AAZ45484	AAZ45484 Fragment
3	221	24.7	222	AAZ45483	AAZ45483 Fragment
4	142.6	16.0	673	ACC44562	ACC44562 Maize gam
5	142.6	16.0	686	AAD57150	AAD57150 Maize gam
6	142.6	16.0	1102	AAZ93520	AAZ93520 27kDa pro
7	142.6	16.0	1839	AAZ93521	AAZ93521 Zein stor
8	141.6	15.8	5173	AAZ08721	AAZ08721 Chimeric
9	141.6	15.8	5360	AAZ08717	AAZ08717 Chimeric
10	141.6	15.8	5392	AAZ08720	AAZ08720 Chimeric
11	141.6	15.8	5622	AAZ08720	AAZ08720 Chimeric
12	132.8	14.9	13680	ADP73931	ADP73931 DNA const
13	49.6	5.5	2000	ADAP73931	ADAP73931 Plasmid p
14	47.2	5.3	19734	ADA71938	ADA71938 Rice gene
15	44	4.9	8056	ABZ10245	ABZ10245 Human imm
16	43.6	4.9	299598	ADQ59380	ADQ59380 Haematopo
17	43	4.8	12069	ABK39931	ABK39931 Human can
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19	42.4	4.7	4165	ABZ10185	ABZ10185 Human imm
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					ABn80136 Human che

C 21	42.2	4.7	8711	4	AAZ46700
C 22	42	4.7	17897	10	ADBS4306
C 23	42	4.7	17897	10	ADBS4178
C 24	42	4.7	17897	13	ADBS9328
C 25	42	4.7	17897	13	ADBS9602
C 26	41.8	4.7	6609	6	ABL33883
C 27	41.8	4.7	6609	6	ABN80247
C 28	41.4	4.6	15592	4	AAZ46453
C 29	41.4	4.6	15592	6	ABL33326
C 30	40.8	4.6	2891	10	ADBS4273
C 31	40.8	4.6	2891	10	ADBS4193
C 32	40.8	4.6	2891	13	ADBS9569
C 33	40.8	4.6	15714	6	ABL33172
C 34	40.8	4.6	15714	6	ABO67057
C 35	40.6	4.5	5349	6	ABL32340
C 36	40.6	4.5	5986	6	ABK28397
C 37	40.4	4.5	1438	6	ABL34376
C 38	40.4	4.5	1438	6	ABL34642
C 39	40.4	4.5	1438	7	ADBS9903
C 40	40.4	4.5	12393	6	ABL33263
C 41	40.2	4.5	1518	6	ABN70493
C 42	40.2	4.5	2000	8	ADA71938
C 43	40	4.5	110000	6	ABO69245_22
C 44	40	4.5	213251	6	ABO67193
C 45	39.8	4.5	15282	6	ABL70190

ALIGNMENTS

RESULT 1	
AAZ45473	
ID AAZ45473 standard; DNA; 894 BP.	
XX AC AAZ45473;	
XX DT 06-APR-2000 (first entry)	
XX DE Nucleotide sequence of the gamma-coixin gene promoter.	
XX KW Gamma-coixin protein; monocotyledonous plant; Coix promoter;	
KW Gene silencing; rice; wheat; oat; barley; rye; sorghum; maize;	
KW Insect resistance; fungal disease resistance; viral disease resistance;	
KW bacterial disease resistance; herbicide resistance; grain composition;	
KW nutrient utilization; mycotoxin reduction; male sterility;	
KW stress resistance; transgenic plant; ss.	
XX OS Coix lacryma-jobi.	
XX PN WO9958659-A2.	
XX PD 18-NOV-1999.	
XX PF 14-MAY-1999; 99WO-US010776.	
XX PR 14-MAY-1998; 98US-00078972.	
XX PA (DEKA-) DEKALB GENETICS CORP.	
XX PI Kriz AL, Luethy MH, Voyles DA;	
DR WPI; 2000-126367/11.	
XX PT New isolated Coix regulatory sequences, used for producing transgenic	
XX PS plants with improved properties.	
XX CS Claim 32; Page 228-229; 238pp; English.	
CC The present sequence represents the promoter of the gamma-coixin gene.	AAZ46700 Tumour su
CC The promoter is used in the method of the invention. The specification	ABbs4306 Pretreate
CC describes a method of preparing a monocotyledonous plant (other than Coix	ABbs4178 Pretreate
CC sp.) expressing a selected gene. The method comprises transforming a	ABbs9328 Oligonuc1
plant cell with construct comprising a selected gene operably linked to a	ABbs9602 Oligonuc1
	ABL33883 Human imm
	ABN80247 Human che
	AAZ46453 Tumour su
	ABL33326 Human imm
	ADBS4273 Pretreate
	ADbs4193 Human lym
	ADbs9569 Oligonuc1
	ABL33172 Human imm
	ABO67057 Human ang
	ABL32340 Human imm
	ABK28397 DNA trans
	ABL34376 Human imm
	ABL34642 Human met
	ADBS9903 Bimulphit
	ABL33263 Human imm
	ABN70493 Streptoco
	ADA71938 Rice gene
	Continuation (23 o
	ABO67193 Listeria
	ABL70190 Chemical1

CC Coix promoter, and then regenerating a monocotyledonous plant which
 CC expresses the gene from the recipient cell. The method can be used to
 CC prevent gene silencing in a monocotyledonous plant. The methods can be
 CC used for transforming monocot plants such as rice, wheat, oats, barley,
 CC rye, sorghum and maize. They can be transformed with genes such as an
 CC insect resistance gene, a fungal disease resistance gene, a viral disease
 CC resistance gene, a bacterial disease resistance gene, a herbicide
 CC resistance gene, a gene affecting grain composition or quality, a
 CC nutrient utilization gene, a mycotoxin reduction gene, a male sterility
 CC gene, a selectable marker gene, a screenable marker gene, a negative
 CC selectable marker gene, a gene affecting plant agronomic characteristics,
 CC and an environment or stress resistance gene. The methods can also be
 CC used for producing transgenic dicot plants such as tobacco, tomato,
 CC potato, soybean and cotton
 CC
 XX
 XX
 SQ Sequence 894 BP, 304 A, 201 C, 170 G, 219 T, 0 U, 0 Other;
 Query Match 100.0%; Score 894; DB 3; Length 894;
 Best Local Similarity 100.0%; Pred. No. 7,4e-254;
 Matches 894; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 1 GGACCGGTACAGACACCACTGGGTGCTCAAGGAGTACCAACTATAGATCCA 60
 Oy 61 TATAGCAGCAAGAACCTGCTGTCTACAAAGCAGAACCAATGCATCACTCAAGG 120
 Db 61 TATAGCAGCAAGAACCTGCTGTCTACAAAGCAGAACCAATGCATCACTCAAGG 120
 Oy 121 AGTACACGCTCTTCTGACTGTCTTCAGAAATGTGGCATTTCTGTGGAAGCATAGCA 180
 Db 121 AGTACACGCTCTTCTGACTGTCTTCAGAAATGTGGCATTTCTGTGGAAGCATAGCA 180
 Oy 181 GTGTAGGTGCTCATTCAAGATATCTCCACAGTAAAGTGAAGATACGGAACGA 240
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 Oy 721 AAGAAACCGTGAAGGCTACACAGCCGCTGCTAGTACAGCAAGAACCAAGAACTGTGCT 780
 Db 721 AAGAAACCGTGAAGGCTACACAGCCGCTGCTAGTACAGCAAGAACCAAGAACTGTGCT 780

Oy 781 AATCGAAGCTATTAATTAACCTAGTATGCTATGCACTTCTCATCACCACATCCATAT 840
 Db 781 AATCGAAGCTATTAATTAACCTAGTATGCTATGCACTTCTCATCACCACATAT 840
 Oy 841 CTTTCACTATTTTACCTTCTCTATCTTCAAGACAGACAGAAAGTGCACACC 894
 Db 841 CTTTCACTATTTTACCTTCTCTATCTTCAAGACAGACAGAAAGTGCACACC 894
 RESULT 2
 AA245484
 ID AA245484 standard; DNA; 412 BP.
 XX
 AC AA245484;
 XX
 DT 06-APR-2000 (first entry)
 XX
 DE Fragment of the gamma-coixin gene promoter.
 XX
 KM Gamma-coixin protein; monocotyledonous plant; Coix promoter;
 KM gene silencing; rice; wheat; oat; barley; rye; sorghum; maize;
 KM insect resistance; fungal disease resistance; viral disease resistance;
 KM bacterial disease resistance; herbicide resistance; grain composition;
 KM nutrient utilization; mycotoxin reduction; male sterility;
 KM stress resistance; transgenic plant; ss.
 XX
 OS Coix lacryma-jobi.
 XX
 PN W0995659-A2.
 XX
 PD 18-NOV-1999.
 XX
 PE 14-MAY-1999; 99WO-US010776.
 XX
 PR 14-MAY-1998; 98US-00078972.
 XX
 PA (DEKA-) DEKALB GENETICS CORP.
 XX
 PI Kriz AL, Luethy MH, Voyles DA;
 XX
 DR WPI; 2000-126367/11.
 XX
 PT New isolated Coix regulatory sequences, used for producing transgenic
 PT plants with improved properties.
 XX
 PS Claim 37; Page 233; 238pp; English.
 XX
 CC The present sequence represents a fragment of the gamma-coixin promoter.
 CC The promoter is used in the method of the invention. The specification
 CC describes a method of preparing a monocotyledonous plant (other than Coix
 CC sp.) expressing a selected gene. The method comprises transforming a
 CC plant cell with construct comprising a monocotyledonous plant which
 CC Coix promoter, and then regenerating a monocotyledonous plant which
 CC expresses the gene from the recipient cell. The method can be used to
 CC prevent gene silencing in a monocotyledonous plant. The methods can be
 CC used for transforming monocot plants such as rice, wheat, oats, barley,
 CC rye, sorghum and maize. They can be transformed with genes such as an
 CC insect resistance gene, a fungal disease resistance gene, a viral disease
 CC resistance gene, a bacterial disease resistance gene, a herbicide
 CC resistance gene, a gene affecting grain composition or quality, a
 CC nutrient utilization gene, a mycotoxin reduction gene, a male sterility
 CC gene, a selectable marker gene, a screenable marker gene, a negative
 CC selectable marker gene, a gene affecting plant agronomic characteristics,
 CC and an environment or stress resistance gene. The methods can also be
 CC used for producing transgenic dicot plants such as tobacco, tomato,
 CC potato, soybean and cotton
 CC
 XX
 XX
 SQ Sequence 412 BP, 147 A, 95 C, 72 G, 98 T, 0 U, 0 Other;
 Query Match 46.0%; Score 411; DB 3; Length 412;
 Best Local Similarity 100.0%; Pred. No. 4,7e-111;
 Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	484	TAAGTATGACGAGGGGGAACAATATCCCTTGCTGAGCGCTAAAGTAAATTACAAAGCCA	5433
Db	2	TAAGTATGACGAGGGGGAACAATATATCTTGCTTGACGCGTAAGTGAATTTACAAAGCCA	61
OY	544	TATATCAACCTTATCTATTAATTAATGAATTCGTATATATACGACGATGATCATCAACA	603
Db	62	TATATCAACCTTATCTATTAATTAATGAATTCGTATATATACGACGATGATCATCAACA	121
OY	604	CCGTACCTGTGAAGGCAACAATAATGAGCCAAGCAAAAATGCAGAAATGAATCATATGAT	6633
Db	122	CCGTACCTGTGAAGGCAACAATAATGAGCCACGCAAAAATGCAGAAATGAATCATATGAT	181
OY	664	GACGAAACGTACACTCGGCTTGCTCACTAAAGTAATGATGAGCATTAATTTGGCAAG	7233
Db	182	GACGAAACGTACACTCGGCTTGCTCACTAAAGTAATGATGAGCATTAATTTGGCAAG	2411
OY	724	AAACCGTGAAAGCTACACAGCCGTCCTAGTAGCACAGGAAACAAGAAATCTGTCTAAT	7833
Db	242	AAACCGTGAAAGCTACACAGCCGTCCTAGTAGCACAGGAAACAAGAAATCTGTCTAAT	301
OY	784	CGAAGCTATAAATTAACCTAGTAGTGCCTATGCACTTCTCCATCACCATAACCATATCTT	8433
Db	302	CGAAGCTATAAATTAACCTAGTAGTGCCTATGCACTTCTCCATCACCATAACCATATCTT	361
OY	844	CAGTCTATTTACTCTCTCTATCTACTCCAGAGGACACAGAAATTCGACACC	894
Db	362	CAGTCTATTTACTCTCTCTATCTACTCCAGAGGACACAGAAATTCGACACC	412

RESULT 3
AAZ45483
ID AAZ45483 standard; DNA; 222 BP.

DT 06-APR-2000 (first entry)

Fragment of the gamma-coixin gene promoter.

KM Gamma-calcin protein; monocytoludonous plant; coix promoter;
KM gene silencing; rice; wheat; oat; barley; rye; sorghum; maize;
KM insect resistance; fungal disease resistance; viral disease resistance;
KM bacterial disease resistance; herbicide resistance; grain composition;
KM nutrient utilization; mycotoxin reduction; male sterility;
KM stress resistance; transgenic plant; ss.

OS Coix lacryma-jobi.

PN W09958659-A2.

PD 18-NOV-1999.

PF 14-MAY-1999; 99WO-US010776.

PR 14-MAY-1998; 98US-00078972.

PA (DEKA-) DEKALB GENETICS CORP.

PI Kriz AL, Luethy MH, Voyles DA;

DR WPI; 2000-126367/11.

PT New isolated Coix regulatory sequences, used for producing transgenic

XX

XX

CC The promoter is used in the method of the invention. The specification
CC describes a method of preparing a monocotyledonous plant (other than Coix
CC sp.) expressing a selected gene. The method comprises transforming a
CC plant cell with construct comprising a selected gene operably linked to a
CC Coix promoter, and then regenerating a monocotyledonous plant which

CC expresses the gene from the recipient cell. The method can be used to
CC prevent gene silencing in a monocotyledonous plant. The methods can be
CC used for transforming monocot plants such as rice, wheat, oats, barley,
CC rye, sorghum and maize. They can be transformed with genes such as an
CC insect resistance gene, a fungal disease resistance gene, a viral disease
CC resistance gene, a bacterial disease resistance gene, a herbicide
CC resistance gene, a gene affecting grain composition or quality, a
CC nutrient utilization gene, a mycotoxin reduction gene, a male sterility
CC gene, a selectable marker gene, a screenable marker gene, a negative
CC selectable marker gene, a gene affecting plant agronomic characteristics,
CC and an environment or stress resistance gene. The methods can also be
CC used for producing transgenic dicot plants such as tobacco, tomato,
CC potato, soybean and cotton

Query Match	24.7%;	Score 221;	DB 3;	Length 222;
Best Local Similarity	100.0%;	Pred. No. 6.3e-55;		
Matches 221; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

OY 674 CACTGGCTTGCATATAAGTGATGATGAGTCATAATATTTGGCAGAACCCTGA 733
| | | | |
Ddb 2 CACTCGCTTGCATATAAGTGATGATGAGTCATAATATTITGGCAAGAACCTGA 61

QY	73	AGCTACACAGCCGTCGTAGTAGCAGCAGAGAAACAAGA	AACTGTGCTATCGAGCTATA	793
Dbb	62	AGCTACACAGCCGTCGTAGTAGCAGCAGAGAAACAAGA	AACTGTGCTATCGAGCTATA	121

Qy	794	AATTAACCCAGTATGCGCTATGACCTTCGCATACACATACCATATCTTCAGCTATT	853
Db	122	AATTAACCCAGTATGCGCTATGACCTTCGCATACACATACCATATCTTCAGCTATT	181

```

Oy      854  ACCTTCTATCTACTCCAGAGACACAGAAGATCGACCC      894
          |||||
Db      182  ACCTTCTATCTACTCCAGAGACACAGAAGATCGACCC      222

```

RESULT 4
ACC44562
ID ACC44562 standard; DNA; 673 BP.

AC	ACC44562;
XX	
DT	02-JUN-2003 (first entry)

DE Maize gamma-zein promoter nucleic acid sequence SEQ ID NO:12.

KW Self-processing plant; processing enzyme; alpha-amylase; grain;

KW mesophilic; thermophilic; hyperthermophilic; transgenic plant; starch;

XX

XX

XX

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XX

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XX

1. **Introduction**
 2. **Background**
 3. **Methodology**
 4. **Results**
 5. **Discussion**
 6. **Conclusion**
 7. **References**
 8. **Appendix**
 9. **Index**
 10. **Table of Contents**
 11. **Figure 1**
 12. **Figure 2**
 13. **Figure 3**
 14. **Figure 4**
 15. **Figure 5**
 16. **Figure 6**
 17. **Figure 7**
 18. **Figure 8**
 19. **Figure 9**
 20. **Figure 10**
 21. **Figure 11**
 22. **Figure 12**
 23. **Figure 13**
 24. **Figure 14**
 25. **Figure 15**
 26. **Figure 16**
 27. **Figure 17**
 28. **Figure 18**
 29. **Figure 19**
 30. **Figure 20**
 31. **Figure 21**
 32. **Figure 22**
 33. **Figure 23**
 34. **Figure 24**
 35. **Figure 25**
 36. **Figure 26**
 37. **Figure 27**
 38. **Figure 28**
 39. **Figure 29**
 40. **Figure 30**
 41. **Figure 31**
 42. **Figure 32**
 43. **Figure 33**
 44. **Figure 34**
 45. **Figure 35**
 46. **Figure 36**
 47. **Figure 37**
 48. **Figure 38**
 49. **Figure 39**
 50. **Figure 40**
 51. **Figure 41**
 52. **Figure 42**
 53. **Figure 43**
 54. **Figure 44**
 55. **Figure 45**
 56. **Figure 46**
 57. **Figure 47**
 58. **Figure 48**
 59. **Figure 49**
 60. **Figure 50**
 61. **Figure 51**
 62. **Figure 52**
 63. **Figure 53**
 64. **Figure 54**
 65. **Figure 55**
 66. **Figure 56**
 67. **Figure 57**
 68. **Figure 58**
 69. **Figure 59**
 70. **Figure 60**
 71. **Figure 61**
 72. **Figure 62**
 73. **Figure 63**
 74. **Figure 64**
 75. **Figure 65**
 76. **Figure 66**
 77. **Figure 67**
 78. **Figure 68**
 79. **Figure 69**
 80. **Figure 70**
 81. **Figure 71**
 82. **Figure 72**
 83. **Figure 73**
 84. **Figure 74**
 85. **Figure 75**
 86. **Figure 76**
 87. **Figure 77**
 88. **Figure 78**
 89. **Figure 79**
 90. **Figure 80**
 91. **Figure 81**
 92. **Figure 82**
 93. **Figure 83**
 94. **Figure 84**
 95. **Figure 85**
 96. **Figure 86**
 97. **Figure 87**
 98. **Figure 88**
 99. **Figure 89**
 100. **Figure 90**
 101. **Figure 91**
 102. **Figure 92**
 103. **Figure 93**
 104. **Figure 94**
 105. **Figure 95**
 106. **Figure 96**
 107. **Figure 97**
 108. **Figure 98**
 109. **Figure 99**
 110. **Figure 100**
 111. **Figure 101**
 112. **Figure 102**
 113. **Figure 103**
 114. **Figure 104**
 115. **Figure 105**
 116. **Figure 106**
 117. **Figure 107**
 118. **Figure 108**
 119. **Figure 109**
 120. **Figure 110**
 121. **Figure 111**
 122. **Figure 112**
 123. **Figure 113**
 124. **Figure 114**
 125. **Figure 115**
 126. **Figure 116**
 127. **Figure 117**
 128. **Figure 118**
 129. **Figure 119**
 130. **Figure 120**
 131. **Figure 121**
 132. **Figure 122**
 133. **Figure 123**
 134. **Figure 124**
 135. **Figure 125**
 136. **Figure 126**
 137. **Figure 127**
 138. **Figure 128**
 139. **Figure 129**
 140. **Figure 130**
 141. **Figure 131**
 142. **Figure 132**
 143. **Figure 133**
 144. **Figure 134**
 145. **Figure 135**
 146. **Figure 136**
 147. **Figure 137**
 148. **Figure 138**
 149. **Figure 139**
 150. **Figure 140**
 151. **Figure 141**
 152. **Figure 142**
 153. **Figure 143**
 154. **Figure 144**
 155. **Figure 145**
 156. **Figure 146**
 157. **Figure 147**
 158. **Figure 148**
 159. **Figure 149**
 160. **Figure 150**
 161. **Figure 151**
 162. **Figure 152**
 163. **Figure 153**
 164. **Figure 154**
 165. **Figure 155**
 166. **Figure 156**
 167. **Figure 157**
 168. **Figure 158**
 169. **Figure 159**
 170. **Figure 160**
 171. **Figure 161**
 172. **Figure 162**
 173. **Figure 163**
 174. **Figure 164**
 175. **Figure 165**
 176. **Figure 166**
 177. **Figure 167**
 178. **Figure 168**
 179. **Figure 169**
 180. **Figure 170**
 181. **Figure 171**
 182. **Figure 172**
 183. **Figure 173**
 184. **Figure 174**
 185. **Figure 175**
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 190. **Figure 180**
 191. **Figure 181**
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 199. **Figure 189**
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 202. **Figure 192**
 203. **Figure 193**
 204. **Figure 194**
 205. **Figure 195**
 206. **Figure 196**
 207. **Figure 197**
 208. **Figure 198**
 209. **Figure 199**
 210. **Figure 200**
 211. **Figure 201**
 212. **Figure 202**
 213. **Figure 203**
 214. **Figure 204**
 215. **Figure 205**
 216. **Figure 206**
 217. **Figure 207**
 218

PT alpha-amylase, useful for producing food products having improved taste or fermentable substrates for ethanol.

PS Claim 22; Page 94; 158pp; English

XX The present invention describes polynucleotides that encode processing
 CC enzymes (e.g. alpha-amylase, pullulanase, alpha-glucosidase, glucose
 CC isomerase, or glucamylase) that are optimised for expression in plants.
 CC The polynucleotides encode mesophilic, thermophilic or hyperthermophilic
 CC processing enzymes, which are activated under suitable conditions to act
 CC upon the desired substrate. Also described are self-processing transgenic
 CC plants and plant parts, e.g. grain, which express one or more of these
 CC enzymes and have an altered composition that facilitates plant and grain
 CC processing. Also described is a method (M) for converting starch to
 CC starch-derived products in a transformed plant part (TPP), by activating
 CC the starch processing enzyme contained in it. Transgenic grain is useful
 CC for preparing maltodextrin. A transformed plant (TP) can be used to
 CC produce food products having improved taste and to produce fermentable
 CC substrates for ethanol and fermented beverages. (M) eliminates the need
 CC to mill or physically disrupt the integrity of plant parts prior to
 CC recovery of starch-derived products. The present sequence represents a
 CC maize gamma-zeln promoter nucleic acid sequence, which is given in the
 CC exemplification of the present invention
 XX

SO Sequence 673 BP; 249 A; 151 C; 123 G; 150 T; 0 U; 0 Other;

Query Match 16.0%; Score 142.6; DB 8; Length 673;

Best Local Similarity 65.3%; Pred. No. 1.ee-31;

Matches 430; Conservative 0; Mismatches 179; Indels 50; Gaps 13;

```

QY 214 CGTAAAGTGTAGGAAATACGAAACGAC---CATTGGCATGTAGAGCTGTATGAATTGG 269
DB 27 CCTAAAGTGTAGGAAACGAAACCAATGCATGGCATGTAAAGCTCCAGAAATTTG 86
QY 270 TGTATTCATACAACTCGCAGAACATCAAAATTTGACGCTCAATGG-ATTGGGTCA 328
DB 87 TTGTATCTTAAACACTCAGAACATCAACAAATTTGACGCTCAATGGGTAA 146
QY 329 GAAACAAATCGTCTCTTGTAGCTTGTACATGAATGATGTAGTCAATGATGACACT 388
DB 147 GAAACAAATCAAAACAAATCTCTGTGTGCAAAAGAAACAGGTGATGATG-CCGAGATC 205
QY 389 GATCCGATCGATATATATATATATATATATATATATATATATATATATATATATAT 448
DB 206 ATACTCATCTGATATATATATATATATATATATATATATATATATATATATATAT 258
QY 449 TATACATCAACAAGTTTGTTCATGAAAAAACAATATATATGACGAGGAGCAATAT 508
DB 259 ATTGCATTAACAAAGATCTTTCATGAAAAAATAA---TAGCCGAGACGACAAAT 314
QY 509 CTTTGTGACGGGTAAAGTGAATTTACAAAGCCATATATCAACTATATATATATAT 568
DB 315 C---CTTGACGTGTAAGTAAATTTACAA---CAAAAAAAGCCATATATGTCAGCTAA 367
QY 569 AGTTGCTATATATATATATATATATATATATATATATATATATATATATATATAT 628
DB 368 ATCTAATTCGTTTACGTATATCAACAACTGTA-----GAAAGCAACAAACT 416
QY 629 GAGCCACGCAAAAATGAGATGATATCATATATATATATATATATATATATATATAT 688
DB 417 GAGCCACGCAAGATACAGATATATATATATATATATATATATATATATATATATAT 466
QY 689 ATAAAGTAATGATGATGATCAATAATATTTGGCAAGAAACCGTGAAGCTACACACGCTC 748
DB 467 GTAAAGAGATGACGATCATATATATATATATATATATATATATATATATATATAT 526
QY 749 GTGATGACACAGGAACAAAGAACTGTG---CTAATGGAAGCTATATATATATATAT 804
DB 527 CTGGGTGGCATTAAGAAACAAAGAAATGTGTATATATATATATATATATATATATAT 586
QY 805 TATGCTATGACATCTTCATACACCACTACCAATATCTCATCTATTTACTCTCTCTTA 863
DB 587 CATGCTGTGATCTTCTCATCACACCA-CTGGGTCTTCAAGACATTAAGCTTTATCTTA 644

```

RESULT 5
 AAD57150

ID AAD57150 standard; DNA; 686 BP.

XX AAD57150;

AC 06-NOV-2003 (first entry)

DE Maize gamma zeln promoter DNA.

KW Thermotolerant phytase; weight gain; animals fed diet; grain processing;

KW nutritive value; transformed plant; anabolic; maize; de.

XX Zea mays.

PN WO2003057248-A1.

XX 17-JUL-2003.

PF 30-DEC-2002; 2002WO-US041787.

PR 28-DEC-2001; 2001US-0344476P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Lanahan MB, Betts S;

DR WPI; 2003-607980/57.

PT Preparing a thermotolerant phytase for preparing animal feed or human
 PT food by expressing in a plant cell an expression cassette comprising a
 PT promoter operably linked to a nucleic acid molecule encoding a
 PT thermotolerant phytase.

PS Claim 11; Page 92-93; 157bp; English.

XX The invention relates to a method for preparing a thermotolerant phytase.
 CC The method comprises expressing in a plant cell an expression cassette
 CC comprising a promoter operably linked to a nucleic acid molecule encoding
 CC a thermotolerant phytase which retains at least 40% activity after 30
 CC minutes at 60plusoc and has a specific activity of greater than 200 U/mg
 CC at pH 4.5 and 37plusoc. The method is useful for preparing a
 CC thermotolerant phytase for preparing animal feed or human food. The
 CC invention is useful for reducing the feed conversion ratio and increasing
 CC weight gain, improving reducing feed conversion ratios or increasing
 CC weight gain of animals fed diets with inorganic phosphate at levels below
 CC 0.45%, minimising dietary requirements of phosphorus in an animal.
 CC enhancing the utilisation of phosphorus present in animal feed, enhancing
 CC organic phosphorus utilisation from organic phosphorus sources in animal
 CC feed, decreasing the phosphate levels in excreta from an animal,
 CC improving the processing of grain, improving the nutritive value of
 CC processed grain product or a method of processing grain, improving the
 CC nutritive value of animal feed and human food, and preparing a
 CC transformed plant which expresses a thermotolerant phytase. The present
 CC sequence is maize gamma zeln promoter DNA used in the exemplification of
 CC the invention
 XX

SO Sequence 686 BP; 252 A; 155 C; 126 G; 153 T; 0 U; 0 Other;

Query Match 16.0%; Score 142.6; DB 9; Length 686;

Best Local Similarity 65.3%; Pred. No. 1.ee-31;

Matches 430; Conservative 0; Mismatches 179; Indels 50; Gaps 13;

```

QY 214 CGTAAAGTGTAGGAAATACGAAACGAC---CATTGGCATGTAGAGCTGTATGAATTGG 269
DB 34 CCTAAAGTGTAGGAAACGAAACCAATGCATGTGATGTAAAGCTCCAGAAATTTG 93
QY 270 TGTATTCATACAACTCGCAGAACATCAAAATTTGACGCTCAATGG-ATTGGGTCA 328
DB 94 TTGTATCTTAAACACTCAGAACATCAACAAATTTGACGCTCAAGGTATTTGGGTAA 153
QY 329 GAAACAAATCGTCTCTTGTAGCTTGTACATGAATGATGTAGTCAATGATGACACT 388
DB 154 GAAACAAATCAAAACAAATCTCTGTGTGCAAAAGAAACAGGTGATGATG-CCGAGATC 212

```


KM ss.
 XX Zea mays.
 OS WO200012681-A1.
 PN 09-MAR-2000.
 PD 25-AUG-1999; 99MO-US020308.
 PF 27-AUG-1998; 98US-0098034P.
 PR 07-JUN-1999; 99US-0137836P.
 XX (RUTE) UNIV RUTGERS STATE NEW JERSEY.
 PA
 XX Meening J, Lai J;
 PT WPI; 2000-237865/20.
 XX
 PT DNA construct used for producing transgenic maize plants that express
 PT high quantities of 10 kilodalton zein seed storage protein encodes delta-
 PT zein operably linked to promoter and to sequence encoding modified 3'
 PT untranslated region.
 PS
 XX Disclosure; Page 49; 54pp; English.
 XX
 CC New DNA constructs are described which encode a delta-zein operably
 CC linked to a promoter and to a modified 3' untranslated region (UTR),
 CC devoid of binding sites for a dzrl negative regulatory protein. The DNA
 CC construct is useful for producing transgenic maize plants that express
 CC high quantities of the 10 kilodalton methionine rich zein seed storage
 CC protein. Overexpression of the zein storage protein in maize seeds
 CC increases the capture of free methionine during plant maturation, which
 CC otherwise would be lost. The transgenic plants are superior to prior art
 CC natural high-methionine variants because they consisently express the 10
 CC kilodalton transgene regardless of the dzrl allelic composition of the
 CC variety
 XX
 SQ Sequence 1839 BP; 595 A; 414 C; 341 G; 489 T; 0 U; 0 Other;
 Query Match 16.0%; Score 142.6; DB 3; Length 1839;
 Best Local Similarity 65.3%; Pred. No. 2.4e-31;
 Matches 430; Conservative 0; Mismatches 179; Indels 50; Gaps 13;
 QY 214 CGTAAAGTGTAGAGTAATCGAAGCAGC-----CATGGCAGTGAAGTGTATGATTTGG 269
 DB 485 CCTAAAGTGTAGAGTAATCGAAGCAGCAGTGTATGAGTGAAGTGTCAAGATTTG 544
 QY 270 TGTATCATATGACCAACTCGCAGAACATCACAATAATGCGCAATG-ATTGGGTCA 328
 DB 545 TTGTATCTTAAACAATCAGAACATCAACCAAAATTGCACTCAAGGATTTGGGTAA 604
 QY 329 GAAACAAATCGTCTCTTGTAGCTTGTACAAATGAATGATGATGATGATGATGATGAT 388
 DB 605 GAAACAAATCAAAATCTCTCTGTGTGCAAAAGAACACGATGATGATGATGATGATGAT 663
 QY 389 GATCCGATGTATATATATGCAAAATGCTCAGCAGAACATTAACAACCAACCCATAC 448
 DB 664 ATACTCATCTGATATACATG-CTTAACAGCTCACAAG--ACATTAACAACAATC-AT 716
 QY 449 TATACATCACAAGTTTGTTCATGAATAAACAATAATATGATGAGAGGAGCAAAATAT 508
 DB 717 ATTGATTTACAAAGATCGTTTCATGAAAAATMAA---TAGCCGAGCAGAGCAAAAT 772
 QY 509 CTTGCTTGAAGCGTAAAGTAATTTACAAAGCCATATATCAACCTATATCTTAATTAATA 568
 DB 773 C-----CTTGAAGTGAAGTAATTTACAA---CAAAAAAAGCCATATGTCAGCTAA 825
 QY 569 AGTTCGTTATATATACGACATATCATCAACAACCGTACTGTTGAAAGGCAACAAAT 628
 DB 826 ATCTAATTCGTTTATACGTAATCAACAACCTGTA-----GAAAGGCAACAAACT 874
 QY 629 GAGCAGCAAAAATGACGAATGAATCATATGATGACGAACGTACACTCGGCTTGTAC 688

DB 875 GAGCAGCAGAGATACAGATGATTCACATBA-----ACCATGAGAGTGTAC 924
 QY 689 ATAAAGTAATGATGACTCTAAATATTTGGCAAGAACCGTGAACCTACACAGCCGTC 748
 DB 925 GTAAGAGAGTGCAGATCATATATATTTGGCAAGAACCATGAAGCTGCTTACAGCGCT 984
 QY 749 GTACGTAGCAGAGAACACAAAGAACTGTG-----CTAATGAAAGCTTAATAATACCTAG 804
 DB 985 CTGGGTGCAATTAAGAACACAAAGAAATTTGTTAATTAATCAAAAGCTTAATAAGCTCG 1044
 QY 805 TATGCTATGACCTTCTCATCAACCACTACCATATCTGATTTAATTAACCTTCTCTA 863
 DB 1045 CAGCCGTGTCAGTCTTCATCAACACCA-CTGGGTCTTACAGACATTAAGCTTATCTTA 1102
 RESULT 8
 AAZ08721
 ID AAZ08721 standard; DNA; 5173 BP.
 XX
 AC AAZ08721;
 XX
 DT 20-OCT-1999 (first entry)
 XX
 DE Chimeric gene construct gz::BHL::gz designated PHP11427.
 XX
 KW Hordeum vulgare; alpha hordochionin; HT12; modification; plant seed;
 KW alteration; endosperm; nutrition; cereal; barley; chimeric gene; 88.
 OS Synthetic.
 XX Hordeum vulgare.
 PN MO9940209-A1.
 XX
 PD 12-AUG-1999.
 PF 27-JAN-1999; 99MO-US002061.
 XX
 PR 09-FEB-1998; 98US-00020716.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 PI Jung R, Beach LR, Dress VM, Rao AG, Ranch JP, Extl DS;
 PI Higgins RK;
 XX WPI; 1999-508509/42.
 DR
 XX
 PT Plant seeds containing elevated preselected amino acid levels, used to
 PT grow cereals.
 PS
 XX Example 2; Page 42-43; 49pp; English.
 XX
 CC The present invention describes a transformed cereal plant seeds
 CC endosperm having an elevated level of at least one preselected amino acid
 CC (aa) compared to a seed from a corresponding untransformed plant, where
 CC the aa is selected from lysine, cysteine, threonine, tryptophan,
 CC arginine, valine, leucine, isoleucine, histidine or their combinations,
 CC and optionally methionine. Plants transformed to express a heterologous
 CC protein that has an elevated content of a preselected amino acid can be
 CC used to grow seeds, especially cereals, that have an endosperm with an
 CC increased content of the preselected amino acid, and therefore having an
 CC increased nutritional value. The transformed cereals can be used in feed
 CC formulations for animals. Transforming plants to have an elevated level
 CC of a preselected amino acid in the endosperm of its seed is advantageous
 CC in production of feed formulations. Feed formulations currently require
 CC supplementation with specific amino acids to provide animals with
 CC essential nutrients, which are necessary for their growth. The methods
 CC increase the nutritional content of seeds without detrimental side
 CC effects such as allergenicity or anti-nutritional quality. The
 CC nutritional content of the seeds is increased whilst maintaining a high
 CC yield. The amount of preselected amino acid in the seed is increased at
 CC least 10-20% by weight to about 10 times greater compared to a
 CC corresponding untransformed seed. The present sequence represents a

CC chimeric gene construct produced in the construction of the HT12 gene;
CC which is derived from the barley (*Hordeum vulgare*) alpha hordeothionin
CC gene and introduces 12 lysine residues into the mature protein
XX
SQ Sequence 5173 BP; 1527 A; 1154 C; 1170 G; 1322 T; 0 U; 0 Other;

SQ Sequence 5173 BP; 1527 A; 1154 C; 1170 G; 1322 T; 0 U; 0 Other;

Query Match	15.8%	Score 141.6	DB 2	Length 5173
Best Local Similarity	63.9%	Pred. No. 7.3e-31		
Matches 441; Conservative	0	Mismatches 199	Indels 50	Gaps 13

OY	214	CGTAAAGGATGAGGAATAACGGAACGAC-----CATTTGCATGTATAGCTGATATGAATTGG	269
Db	1550	CCTTAAGGTGTGAGGAACAACGAAAGAACGATGATGGCATGTAAAGCTCCAAGAATTTG	1605
OY	270	TGTTATCCATATCAACAACTCGCAGAAATCATCAAAAATTGCACGTCAATGG--ATTGGGTCA	328
Db	1610	TTGTATCTTTAACTACAGAAATATCAACCAAAATTGCACGTCAAGGGATTTGGGTAA	1666
OY	329	GAAGCAAAATCGTCTCTCTTTAGCTTGTACAAATGAAGTATGGTGAATGATGACACT	388
Db	1670	GAAGCAAAATCAAAACAAATCCTCTCTGTGTGCAAGAAACACGGTGAATGATG--CGAATATC	1722
OY	389	GATCCGATCTGATATATATATGCCAAATACTCACACGACAACTTTACAAACCAACCCATAC	448
Db	1729	ATACTCATCTATATATACATG--CTTACAGCTCACAG--ACATTTCAAAACAATC---AT	1781
OY	449	TATACATCAACAAAGTTGGTTTCATGAATAAAACAAATAGTATGACGAGGGGACAAATAT	508
Db	1782	ATTGCATTACAAAGATCGTTTCATGAAATAAATAA---TAGCCGACAGACAAAAAT	1837
OY	509	CCTTGCTTGACGCGTAAAGATGAATTTACAAAGCCATATATCAACTATATCTAATTATA	568
Db	1838	C-----CTTGACGTGTAAAGTAATTACAA---CAAAAAAAAAAGCATATGTCAAGCTAA	1890
OY	569	AGTTGCTTATATATPACGACGATGATATCAACAACCGTACTGTGAAGGCAACAAAT	628
Db	1891	ATCTAATTCGTTTAACTAGATATCAACAACCTGTAT-----GAAGGCAACAAACT	1939
OY	629	GAGCCAGCGCAAAATGCGAATGGAATCCATATGATGACGAACGTACACTCGGCTTGTAC	688
Db	1940	GAGCCAGCGCAAAAGTACGAATGATTTCCAGATGA-----ACCATTCACGCTGATC	1988
OY	689	ATTAAGTGAATGATGAGTCATATTAATTTGGCAAGAAACCGTGAAGAGCTACACAGCCGTC	748
Db	1990	GTTAAAGAGTGAAGATCATATATACATTTGGCAGAAACCATGAAGCTGCTTACAGCCGT	2048
OY	749	GTCAGTAGCAGAGAACCAAGAAATCTGTG-----CTAATCGAAGCTATTAATTAACCTTAG	804
Db	2050	ATCGGTGCGATTAAGAACCAAGAAATTTGTATTAATTAATCAAAAGTATTAATTAACGCTG	2109
OY	805	TATGCTTATGCACTTTCTTCATACGACATACCACTATCTTTCAGTCTAATTACCTTCTAT	864
Db	2110	CATCCCTGTGTGCACTTCTTCATACACCA--CTGGGTCTTCAGACCATTAAGCTTATCTAC	2168
OY	865	CTACTCCAGAGACACGAAGATGACACCC	894
Db	2169	TTCCAGAGCGCAAGAAAGATCCGATGACACCC	2198

RESULT 9
AAZ08717
ID AAZ08717 standard; DNA; 5360 BP.

AC AA208717;

DT 20-OCT-1999 (first entry)

DE Chimeric gene construct gz::HT12::gz expression vector.

KW Hordeum vulgare; alpha hordochionin; HT12; modification; plant seed alteration; endosperm; nutrition; cereal; barley; chimeric gene; ss

OS Synthetic.

OS **Hordeum vulgare**

PN WO9940209-A1

PD 12-AUG-1999

PF 27-JAN-1999; 99WO-US002061.

PR 09-FEB-1998; 98US-00020716.

PA (PION-) PIONEER HI-BRED INT INC
...

PI Jung R, Beach LR, Dress VM, Rao AG, Ranch JP, Ertl DS;

2000

2000

grow cereals.

PS Example 2; Page 36-37; 49pp; English

The present invention describes a transformed cereal plant seeds endosperm having an elevated level of at least one preselected amino acid (aa) compared to a seed from a corresponding untransformed plant, where the aa is selected from lysine, cysteine, threonine, tryptophan, arginine, valine, leucine, isoleucine, histidine or their combinations, and optionally methionine. Plants transformed to express a heterologous protein that has an elevated content of a preselected amino acid can be used to grow seeds, especially cereals, that have an endosperm with an increased content of the preselected amino acid, and therefore having an increased nutritional value. The transformed cereals can be used in feed formulations for animals. Transforming plants to have an elevated level of a preselected amino acid in the endosperm of its seed is advantageous in production of feed formulations. Feed formulations currently require supplementation with specific amino acids to provide animals with essential nutrients, which are necessary for their growth. The methods increase the nutritional content of seeds without detrimental side effects such as allergenicity or anti-nutritional quality. The nutritional content of the seeds is increased whilst maintaining a high yield. The amount of preselected amino acid in the seed is increased at least 10-20% by weight to about 10 times greater compared to a corresponding untransformed seed. The present sequence represents a chimeric gene construct g2::H12::g2 expression vector produced in the construction of the H12 gene, which is derived from the barley (*Hordeum vulgare*) alpha hordeothionin gene and introduces 12 lysine residues into the mature protein.

SQ Sequence 5360 BP; 1557 A; 1212 C; 1208 G; 1383 T; 0 U; 0 Other;

Query Match	15.8%	Score 141.6	DB 2	Length 5360
Best Local Similarity	63.9%	Pred. No. 7.4e-31		
Matches 441; Conservative	0	Mismatches 199	Indels 50	Gaps 13

Oy	214	CGTAAAGTGAAGAGTAATCGGAACGAC---	CATTGGCANTGAGCTGTATGAATTGG	269
Db	1550	CTTAAAGTGGAGAGAAACACGAAAAGAAC	CCATGCAATTGGCAGTAAAGCTCCAAAGATTGG	1605
Oy	270	TGTTATCCATCAACAACCTCGCAGAACATCA	ACCAAAATTGCACGTCATAGG-ATTGGGTCA	328
Db	1610	TTGTATCCTTACAACTCACAGAACATCAAC	CAAAATTGCACGTCACAGGGATTTGGGTAA	1665
Oy	329	GAACCAAAATCGTCTCCCTTGTAGCTTTGA	CAATGAAGTGATGCTGATGATCACT	388
Db	1670	GAACCAATCAAAACAAATCCTCTCTGTGTG	CAAGAAACACCGTAGTCATG-CCGAGATC	1728
Oy	389	GATCCGATCTGATATATATATGCGCAATAT	AGCTCACACGACCAACATTACAAACACCCCATAC	448
Db	1729	ATACTCACTGTATATACATG-CTTACAGCT	CACAAG---ACATTACAAACAACTC---AT	1781
Oy	449	TATACATCACAAAGTTGTTTCATGA	AAAAACAAATAAGTATGCAAGAGGGGACCAATAT	508
Db	1782	ATTGCATTACCAAAAGTCGTTTCATGA	AAAAAATTTAAA---TAGGCGGACAGGACCAAAAT	1837

RESULT 11
AAC86506
ID AAC86506 standard; DNA; 5622 BP.
XX
AC AAC86506;
XX
DT 19-MAR-2001 (first entry)
XX
DE DNA construct comprising a maize promoter and Agrobacterium ipt gene.
XX
KM temporal gene expression; spatial gene expression; plant seed;
KM cytokinin modulating gene; transgenic plant; seed size; stress tolerance;
KM yield stability; tip kernel abortion; seed set; isopentenyl transferase;
KM ipt; ss.
XX
OS Synthetic.
OS Zea mays.
OS Agrobacterium tumefaciens.
XX
FN MO200063401-A1.
XX
PD 26-OCT-2000.
XX
PF 13-APR-2000; 2000WO-US0009943.
XX
PR 16-APR-1999; 99US-0129844P.
XX
PA (PTON-) PIONEER HI-BRED INT INC.
XX
PI Habben JE, Zinselmeier C, Tomes D;
XX
DR WPI; 2000-672743/65.
XX
XX Novel recombinant DNA construct useful for producing transgenic plants
FT having enhanced levels of cytokinin expression, improved stress tolerance
FT and yield stability.
XX
PS Disclosure; Page 67-69; 76pp; English.
XX
XX The present sequence represents a recombinant DNA molecule of the
CC invention. It comprises, in this order, a maize promoter, an
CC Agrobacterium isopentenyl transferase (ipt) gene fragment, and a maize
CC terminator. The DNA molecules of the invention comprise a genetic
CC construct consisting of a promoter directing temporal and/or spatial gene
CC expression in plant seed operatively linked to a cytokinin modulating
CC gene. The recombinant DNA molecules are useful for producing fertile,
CC transgenic plants capable of regulated expression of a cytokinin
CC modulating gene in developing seeds. They are also useful for improving
CC stress tolerance and yield stability in plants. The preferential
CC expression of recombinant DNA molecules of the invention occurs about 14-
CC 25 days after pollination. The transgenic plants thus produced have
CC enhanced levels of cytokinin expression exhibit improved seed size,
CC decreased tip kernel abortion and increased seed set during unfavourable
CC environmental conditions
XX
SQ Sequence 5622 BP; 1546 A; 1295 C; 1189 G; 1592 T; 0 U; 0 Other;

Query Match 15.8%; Score 141.6; DB 3; Length 5622;
Best Local Similarity 63.9%; Pred. No. 7,5e-31;
Matches 441; Conservative 0; Mismatches 199; Indels 50; Gaps 13;

QY 214 CGTAAAGTATGAGGATACGAAACGAC----CATTGGCATGTAGCTGTATGTAATTGG 269
DB 876 CCTAAAGTGTGAGGAAACGAAAGAACCATGTGCGATGTAAAGCTCCAGAAATTGG 935
QY 270 TGTATTCATACCAACAACTCGAGAACATCAAAATTGCGATGATG--ATTGGGGTCA 328
DB 936 TTGTAATCTTAAACAATCAAGAACATCAACCAAAATTGCAAGTAAAGGATTTGGGTTAA 995
QY 329 GAAACAAATCGTCTCTTGTAGCTTGTACAAATGAAGTATGATGATGATGATGATGATGATG 388
DB 996 GAAACAAATCAAAATCTCTCTGTGTGCAAAAGAAACACGATGATGATG--CCGAGATC 1054

QY 389 GATCCGATCTGATATATATATGCCCATAATAGCTCACAGCAACATTAACAACCCCATAC 448
DB 1055 ATACTCATCTGATATATCATG--CTTACAGCTCACAG--ACATTACAAAGCACTC---AT 1107
QY 449 TATACATCAACAAGTTTGTTCATGAAAACAAATATAGTATGACAGAGGGACATATAT 508
DB 1108 ATTGCATTACAAAGATGTTTCATGAAAAATATAAA-----TAGGCCGACAGACAAAAT 1163
QY 509 CCTTGCTGAGCGCTTAAGTGAATTTTCAAGACCATATATCACTATATCTATATATATA 568
DB 1164 C---CTTGAAGTGTAAAGTAAATTTTCA--CAAAAAAAGCCATATGTCAAGCTTA 1216
QY 569 AGTTGTAATATATACCAACGATATCATCAACCGTACCTGTGAAGGCAACAAAT 628
DB 1217 ATCTAATTCGTTTACGTATGATCAACAACCTGTG-----GAAAGCAACAAACT 1265
QY 629 GAGCCACGCAAAAAATGCAAGATGAATCATATGATGACGAACGTACACTCGGCTTGCTAC 688
DB 1266 GAGCCACGCAAGATGACGAATGATTCAGATGA-----ACATGACGCGTAC 1315
QY 689 ATAAAGTATGATGATGATCAATAATTTTGGCAAGAAACCGTGAAGCTACACAGCGTC 748
DB 1316 GTAAAGAGAGTGAAGAGTCAATATATGTCAGAAAGAAACCATGAGCTGCTACAGCGCT 1375
QY 749 GTCAAGTACAGAGACAGCAAGAAACTGTG---CTAATGAGCTATTAATTAACCTAG 804
DB 1376 ATCGGTGATTAAGACACAAAGAAATGTGTTAATTAATCAACCTATTAATTAACGCTCG 1435
QY 805 TATGCTTATGACCTTCTCATACACCACTATATCTTCACTATATCTTCTAT 864
DB 1436 CATGCTGTGCACTTCTCATACACCA--CTGGGTCTTGACACATTAGCTTATCTAC 1494
QY 865 CTACTCCAGAGACACAGAAAGATGACACC 894
DB 1495 TCCAGACGCGAAGAAACCGATGACACC 1524

RESULT 12
ADP73931
ID ADP73931 standard; DNA; 13680 BP.
XX
AC ADP73931;
XX
DT 09-SEP-2004 (first entry)
XX
DE Plasmid PDAB8505, SEQ ID NO:85, encoding mAb HX8 (both chains).
XX
KM Transgenic plant; immunoglobulin production; recombinant production;
KM glycosylation; fucose; glycan; virulence; immunotherapy; maize;
KM gamma-zeln promoter; rice; actin promoter;
KM phosphinothricin acyltransferase; PAT; mouse; leader sequence;
KM herpes simplex virus; HSV1; HSV2; human; monoclonal antibody HX8; IGA;
KM heavy chain; light chain; codon optimised; plasmid; PDAB8505; cyclic;
KM circular; ds.
XX
XX Zea mays.
OS Mus sp.
OS Homo sapiens.
OS Oryza sativa.
OS Chimeric.
OS Synthetic.
OS Unidentified.
XX
XX Key misc_feature
FT 424..1589
FT Location/Qualifiers
FT /*tag= a
FT /label= S&R
FT /note= "Scaffold attachment region. Also referred to as
FT MAR (matrix association region)"
FT 1673..3175
FT /*tag= b
FT /note= "Maize gamma-zeln promoter"
FT 3178..4671
FT CDS

```
FT      /tag= d
FT      /product= "Heavy chain of human anti-HSV1/HSV2 monoclonal
FT      IGA antibody HX8 (with mouse leader sequence)"
FT      3178..3234
FT      sig_peptide
FT      /tag= C
FT      /note= "Mouse leader sequence"
FT      3235..4668
FT      mat_peptide
FT      /tag= e
FT      /product= "Mature HX8 heavy chain"
FT      4678..5045
FT      3'UTR
FT      /tag= f
FT      /note= "Maize per5 3'UTR"
FT      5157..6659
FT      promoter
FT      /tag= g
FT      /note= "Maize gamma-zein promoter"
FT      6662..7363
FT      CDS
FT      /**tag= i
FT      /product= "Heavy chain of human anti-HSV1/HSV2 monoclonal
FT      IGA antibody HX8 (with mouse leader sequence)"
FT      6662..6718
FT      sig_peptide
FT      /note= h
FT      /tag= h
FT      /product= "Mouse leader sequence"
FT      6719..7360
FT      mat_peptide
FT      /tag= j
FT      /product= "Mature HX8 heavy chain"
FT      7370..7737
FT      3'UTR
FT      /tag= k
FT      /note= "Maize per5 3'UTR"
FT      7889..9258
FT      promoter
FT      /tag= l
FT      /note= "Rice actin promoter/intron"
FT      9261..9815
FT      CDS
FT      /tag= m
FT      /product= "Phosphoinositide acyltransferase (PAT)"
FT      /note= "The PAT coding region is given in the
FT      specification as positions 9260-9820"
FT      9831..10162
FT      3'UTR
FT      /tag= n
FT      /note= "Maize lipase 3'UTR"
FT      10229..11394
FT      misc_feature
FT      /tag= o
FT      /label= SAR
FT      /note= "Scaffold attachment region. Also referred to as
FT      MAR (matrix association region)"
FT      PN      WO2004050838-A2.
FT      XX      17-JUN-2004.
FT      PD      28-NOV-2003; 2003WO-US037905.
FT      PF      27-NOV-2002; 2002US-0429385P.
FT      PR      (DOWC ) DOW CHEM CO.
FT      PA      (DOWC ) DOW AGROSCIENCES LLC.
FT      PA      (EPIC-) EPICYTE PHARM INC.
FT      XX      Briggs K, Giancy T, Hein MB, Hartz AC, Karnoup AL, Anderson WHK;
FT      PI      Paredy D, Petolino J, Rubin-Wilson B, Taylor D, Roberts JL;
FT      DR      WPI; 2004-461111/43.
FT      DR      P-PSDB; ADP73848, ADP73856.
FT      XX      Novel plant-produced immunoglobulin having glycopeptide or glycan profile
FT      PT      with reduced fucosylation, useful for treating herpes simplex virus
FT      infection.
FT      PS      Claim 69; SEQ ID NO 85; 212pp; English.
FT      XX      The invention relates to the production of immunoglobulins in plants,
FT      CC      wherein at least a portion of the glycans attached to the immunoglobulins
FT      CC      lack fucose. The immunoglobulins produced can be of any class (i.e., IgG,
FT      CC      IgA, IgM, IgE or IgD) and is especially an anti-herpes simplex virus
```

```
CC      (HSV) antibody or an anti-alpha/beta3, alpha/beta5 dual integrin
CC      antibody. The invention also relates to constructs, plasmids and vectors
CC      for producing the immunoglobulins; transformed plant cells; calli; plant
CC      tissues and whole plants for producing the immunoglobulins; methods for
CC      producing the immunoglobulins, the immunoglobulins thus produced; and the
CC      use of such immunoglobulins. The immunoglobulins of the invention may be
CC      used to treat HSV infection or tumor angiogenesis. The invention
CC      provides the advantages of antibody production in plants, such as large
CC      scale production, reduced costs, and elimination of pathogenic
CC      contaminants such as viruses and prions, with a simplified (i.e., non-
CC      plant-specific) glycosylation profile which reduces the risk that the
CC      immunoglobulin may not be functional in animals. The present sequence
CC      represents the plasmid pDB8505, which contains codon optimised DNA
CC      sequences encoding the heavy and light chains of the human anti-HSV1/HSV2
CC      monoclonal IGA antibody HX8 each of which are fused to mouse leader
CC      sequences. Both heavy and light chain fusion genes are under the control
CC      of maize endosperm-specific gamma-zein promoters. The plasmid also
CC      contains a phosphoinositide acyltransferase (PAT) gene under the control
CC      of a rice actin promoter.
XX      Sequence 13680 BP; 3886 A; 3069 C; 2934 G; 3788 T; 0 U; 3 Other;
XX      Query Match      14.9%; Score 132.8; DB 12; Length 13680;
XX      Best Local Similarity 64.1%; Pred. No. 4,4e-28;
XX      Matches 442; Conservative 0; Mismatches 197; Indels 51; Gaps 14;
XX      214  CGTAAAGTATGAGGAATACGAAACGAC---CATTGGCATGTAGAGCTGTATGAAATTGG 269
XX      2530 CCTAAAGTGTGAGGAACAGAAACAAACATGATGGCATGTGAAAGCTCCAGAAATTGG 2589
XX      270  TGTATTCATTAACAACCTGCGAGAACATCAAAATTTGACGCTCAATGG-ATTGGGTCA 328
XX      2590 TTGTATCTTAACAACATCAAGAAACATCAAAATTTGACGCTCAAGGGTATTGGGTAA 2649
XX      329  GAAACAAATCGTCTCCTTGAGCTTGATACATGAAGATGATGAGATGAGATGAGTCAACT 388
XX      2650 GAAACAAATCAACAAACCTCTCTGTGTGAAAGAAACAGGGTATGATG-CCGAGATC 2708
XX      389  GATCCGATGTATATATATATGCAAAATGCTCACAGCAACATTACAAACCCCATAC 448
XX      2709 ATACTCATCTGATATATCATG-CTTACAGCTCACAG---ACATTACAAACATC---AT 2761
XX      449  TATACATCAAAAGTTTGTTCATGAAAAAAACAATATAGTATGACAGGGGACAAATAT 508
XX      2762 ATTGCATTAACAAAGATGTTTCAAGAAAAATATAA---TAGCGCGAGACGACAAAAAT 2817
XX      509  CCTTGCTTGAAGCGTAAAGTGAATTTTCAAGACCATATATCAACCTTATCTAATTATA 568
XX      2818 C---CTTGAAGTGAAGTAAATTTACAA---CAAAAAAAAGCCATATGTCAAGCTAA 2870
XX      569  AGTTCGTTATATATACGACGATGATCATCAACACCGTACTGTGAAAGGCAACAAAT 628
XX      2871 ATCTAATTCGTTTACGTAATATCAACAACTGTG-----GAAGCAACAAAACT 2919
XX      629  GAGCCAGCAAAAATGAGAAATGATATCATATGATGACGAACGTACCTCGGCTGTAC 688
XX      2920 GAGCCAGCAGAAAGTACAGATGATTCAGATGA-----ACCATGAGCGTGTAC 2969
XX      689  ATAAAGGATGATGATCATTAATATTGGCAAGAAACCGTGAACCTACACAGCGTTC 748
XX      2970 GTAAAGAGATGACGATCATATATCATTTGGCAAGAAACGATGAAGTGTGCTTACAGCGT 3029
XX      749  GTCAAGTACAGAGAACACAAAGAACTGTGC---TAATGAAAGCTTAATAATACCTAG 804
XX      3030 CTGGTGGCATA-GAACAAGAAATGTGTATTAATTAAGCTTAATAATAGCTCG 3088
XX      805  TATGCTATGCACTTCTTCATCAACCACTACCAATATCTTGAAGTATTAATCTTCTAT 864
XX      3089 CATGCTGTGCACTTCTTCATCAACCA-CTGGGTCTTCAGACATTAGCTTATCTATAC 3147
XX      865  CTACTCCAGAGAGACAGAAAGATGACACC 894
XX      3148 TCAGAGCGGAGAGAAACCCGATCGACACC 3177
DB
```


CC diseases. The present sequence is a gene of the invention
XX Sequence 19734 BP; 6048 A; 167 C; 3900 G; 9619 T; 0 U; 0 Other;
SQ
Query Match 5.3%; Score 47.2; DB 6; Length 19734;
Best Local Similarity 46.6%; Pred. No. 0.011;
Matches 151; Conservative 0; Mismatches 173; Indels 0; Gaps 0;
QY 388 TGATCCGATCTGATATATATGCAAAATAGCTCACACGCAACCTTACAAACACCCCTTA 447
DB 4680 TAAACCTTAAAAAATTAATAATTAATAACCTTAATTGCGCAGCTACCTCCAAACCCCAA 4621
QY 448 CTATACATCACAAAGTTGTTTCATGAAAAACAATAATAGATGAGAGGAGCAATTA 507
DB 4620 CGACAAAACAAACCCCATCTTTAAAAAATAAATTAACCTTAATTTCAATCTTAAT 4561
QY 508 TCCTTGCTGACGGGTAAAGTAAATTTTCAAAAGCATATATCAATCTATCTATTAAT 567
DB 4560 TCTACATTTACTATTAATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4501
QY 568 AAGTTCTTATATATGACGAGATGATCATCAACACCGTACCTGTGAAGGCAACAAA 627
DB 4500 TTCACTTATTAATTAACCAAAATTAATCTTCCAAAATCTATTAATAAATTAATAA 4441
QY 628 TGAGCCACGCAAAATGACAGATGATCATATGATGACGACGACCTGGCTTCTTA 687
DB 4440 AAAAATAATTAATCAATTTTAACTATTAATTAATTAATTAATTAATTAATTAATTA 4381
QY 688 CATTAAGTAAATGATGATCATTA 711
DB 4380 AATAATCTTAATCAATTAATTTTA 4357
RESULT 15
AB210245/C
ID AB210245 standard; DNA; 8056 BP.
XX
AC AB210245;
XX
DT 16-JAN-2003 (first entry)
XX
DE Haematopoietic cell proliferation disorder related DNA sequence #385.
XX
KW Human; haematopoietic cell proliferation disorder; cytostatic;
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW cytosine methylation state; gene; ds.
XX
OS Homo sapiens.
XX
PN WO20027272-A2.
XX
PD 03-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-EP003401.
XX
PR 26-MAR-2001; 2001US-0278333P.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E, Pelet C;
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
PI Schwope I, Ziebarth H;
XX
DR WPI; 2003-018942/01.
XX
PT Detecting and differentiating between hematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX
PS Claim 28; SEQ ID NO 385; 117bp; English.
XX
CC The present invention describes a method for detecting and

CC differentiating between haematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. AB209861 to AB21118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used: for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of haematopoietic cell proliferation disorder related DNA
CC sequences. The nucleotide sequences from the present invention can also
CC be used for detecting a predisposition to, differentiation between
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC haematopoietic cell proliferative disorders. The present method enables a
CC highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients
SQ
Sequence 8056 BP; 1858 A; 0 C; 2116 G; 4082 T; 0 U; 0 Other;
XX
Query Match 4.9%; Score 44; DB 8; Length 8056;
Best Local Similarity 47.5%; Pred. No. 0.067;
Matches 131; Conservative 0; Mismatches 145; Indels 0; Gaps 0;
QY 385 CACTGATCCGATCTGATATATATGCAAAATAGCTCACACGCAACATTACAAACACCCC 444
DB 2870 CACTTCCCAAAAAAATTTCAATATCTTAACACATCAAAAAAATCTTCAAAAAACAA 2811
QY 445 ATACTATACATCACAAAGTTGTTTCATGAAAAACAATAATAGATGACGAGGGCA 504
DB 2810 ATCTTAACAACAACAAAAAATATCCCAATTAACAAATAATCTCCCAATCAAAAA 2751
QY 505 TAATCTTGCTGACGGGTAAAGTAAATTTTCAAAAGCATATATCAACCTATCTAAT 564
DB 2750 AATCACATCTTAAATCAAAATTTATTCATTCATTAATAAATATCCACCACTACTTA 2691
QY 565 AATAAGTTCGTTATATATTAAGCAGATGATCATCAACACCGTCTGAAAAGGCA 624
DB 2690 ACAAAATTTGATAATATCAACAATAATTAACAACCACTACTTAATAATCAACAAAAT 2631
QY 625 AATGAGCCACGCAAAATGCAAGATGATCATAT 660
DB 2630 CTAAACCAAAACAAACCCCTATTCATCTCAAAAT 2595

Search completed: September 24, 2005, 15:04:54
Job time : 550 secs

Best Local Similarity 58.6%; Pred. No. 3,4e-25;
Matches 401; Conservative 0; Mismatches 234; Indels 52; Gaps 11;

```
QY 214 CTTAAAGTATGAGGAATACGGAACGAC---CATTGGCATGTAGACCTGTATGATTTGG 269
    |||||
DB 479 CTTAAAGTGTGAGGAACAGCAACCAATGATGTGGCATGTAAAGCTCCAGAAATTTGG 538
    |||||
QY 270 TGTATTCATACCAACACTGGCAGACATCAACAAATTTGACGTCANTGG-ATTGGGTCA 328
    |||||
DB 539 TTGTATCTTAACTCACTCAAGAACATCAACCAAAATTTGACGTCAGGGGATTTGGGTAA 598
    |||||
QY 329 GAAACAAATGCTCTCTTGTAGCTTGTACATGAAAGTGTAGTCACTGAGTCACACT 388
    |||||
DB 599 GAAACATCAACAAATCTCTCTGTGTGCAAGAAACACGCTGAGTCATG-CCGAGATC 657
    |||||
QY 389 GATCCGATCTGTATATATGCAAAATGCTCAACGACAACTTACAAACACCCCATAC 448
    |||||
DB 658 ATACTCATCTGATATACATG-CTTACAGCTCACAAG--ACATTACAAACAATC--AT 710
    |||||
QY 449 TATACATCACAAGTTGTTTCATGAAACAAATAGTATG-CAGGAGGGGACAAATTA 507
    |||||
DB 711 ATTGCATTACAAAGATGTTTCATGNNNNNTAAATATGGCCGACAGGACNNNNNTCCTT 770
    |||||
QY 508 TCTTGTCTTGCAGCGTAAAGTAAATTTACAAAGCCATATATCAACTATATCTAATTAAT 567
    |||||
DB 771 GAGCTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 827
    |||||
QY 568 AAGTTCCTTATATATACGACGATGATCATCAACACCGTACCTGTGAAAGGCAACAAA 627
    |||||
DB 828 -----CGTTTACGTATGATCAACACCTGTAGAGGCAACAAAAC 867
    |||||
QY 628 TGAAGCAAGCAAAATCGAAGATGATCCATATGATGACGAAGTACACTGCGTGTGTA 687
    |||||
DB 868 TGAAGCAAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 917
    |||||
QY 688 CATTAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 747
    |||||
DB 918 CTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 977
    |||||
QY 748 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 803
    |||||
DB 978 TCTGCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1037
    |||||
QY 804 GTATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 863
    |||||
DB 1038 GATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1096
    |||||
QY 864 TCTATCTCAGAGACACAGAAAGATGACACC 894
    |||||
DB 1097 CTCAGAGCGCAGAAAGACCGGATGACACC 1127
    |||||
```

RESULT 2
CC365454/c 848 bp DNA linear GSS 16-MAY-2003
LOCUS PUHXY9TB ZM 0.6_1.0_KB Zea mays genomic clone ZMBRta475G05,
DEFINITION genomic survey sequence.

ACCESSION CC365454
VERSION CC365454.1 GI:30834854
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
AUTHORS Benneick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Whiteclaw,C.A., Quackenbush,J., Van Aken,S., Utechtack,T.,
1 (bases 1 to 848)
clade; Panicoidae; Andropogoneae; Zea.

TITLE Zea mays
JOURNAL Maize Genomics Consortium
COMMENT Unpublished (2003)
Contact: Cathy Whiteclaw
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whiteclaw@tigr.org
Seq primer: TR
Class: sheared ends.

FEATURES
source
1. 848
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMBRta475G05"
/note="Vector: pCR4-T0B0; Site 1: EcoRI; 0.6-1.0 Kb high
COT selected genomic DNA library"

ORIGIN

Query Match 14.1%; Score 125.8; DB 8; Length 848;
Best Local Similarity 62.2%; Pred. No. 2.1e-24;
Matches 401; Conservative 0; Mismatches 197; Indels 47; Gaps 11;

```
QY 255 AGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 314
    |||||
DB 847 AGCTCAAGAAATTTGTGTATCTTAACTCACTCAACAAATCAACCAAAATGACAGTC 788
    |||||
QY 315 AATGG-ATTGGGTGAGAAACAAATCGTCTCTGTAGCTTGTACATGAATGAATGATGTA 373
    |||||
DB 787 AAGGATTTGTGGTAAAGAAACATCAACAAATCTCTGTGTGCAAGAAACCGGTGA 728
    |||||
QY 374 GTCTAGATGACACTGATCCGATCTGATATATATGCAAAATAGCTCAGACAAATTA 433
    |||||
DB 727 GTCTAGCCGAGATCAT-CTCATCTGATATACATGCTTAC-AGCTCAAGAC---ATTA 673
    |||||
QY 434 CAACCAACCCCATATATATATATATATATATATATATATATATATATATATATATATAT 493
    |||||
DB 672 CAACCAATC---ATATGATATTAACAAAGATCTGTTTCATGAAATTAATTAATAG---GCC 620
    |||||
QY 494 GAGGAGCAATATATCTTCTGCTGACCGGTAAGTGAATTTACAAACCATATATCAACC 553
    |||||
DB 619 GAGACGACAAAAATC---CTTGACGTGTAAGTAAATTTACAAACAAAGGCAATTA 564
    |||||
QY 619 GAGACGACAAAAATC---CTTGACGTGTAAGTAAATTTACAAACAAAGGCAATTA 564
    |||||
QY 554 TATATCTAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 613
    |||||
DB 563 TGTCAAGCTAATATATATATGTTTATGTA-----GATCAACAACTGTA 519
    |||||
QY 614 GAAAGCAACAAATGAGCCACGCAACAAATGAGATGATGATGATGATGATGATGATGATG 673
    |||||
DB 518 GAAAGCAACAAATGAGCCACGCAACAAATGATGATGATGATGATGATGATGATGATGATG 469
    |||||
QY 674 CACTCGGCTGTCTATATAGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 733
    |||||
DB 468 CCATGAGAGTGTCTACGTAAGAGAGTGAACGATATATATATGTCAGAAACCAATGAA 409
    |||||
QY 734 AGTACACACCGCTGTCTAGTACAGCAACAACTGCTG---CTAATGAAAGC 789
    |||||
DB 408 GCTGCTTACAGCCCTCTCGGTGATGATGATGATGATGATGATGATGATGATGATGATG 349
    |||||
QY 790 TATAATTAACCTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 849
    |||||
DB 348 TATAATTAACCTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 290
    |||||
QY 850 ATTTACCTTCTATCTATCTACTCCAGAGGACACAGAAAGTCCAGACC 894
    |||||
DB 289 ATTAGCTTTATCTATCTCAGAGCGCAGAAAGACCGGATGACACC 245
    |||||
```

RESULT 3
CG076785/c 796 bp DNA linear GSS 20-AUG-2003
LOCUS PUERJ9TB ZM 0.6_1.0_KB Zea mays genomic clone ZMBRta056M14,
DEFINITION genomic survey sequence.
ACCESSION CG076785

VERSION	CG076785.1	GI:33955223
KEYWORDS	GSS:	
SOURCE	Zea mays	
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	
REFERENCE	Whitefaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T., Renick,A., Frazer,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennetzen,J.	
AUTHORS	Maize Genomics Consortium	
TITLE	Unpublished (2003)	
JOURNAL	Contact: Cathy Whitelaw	
COMMENT	TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA Tel.: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@cigr.org Seq primer: TR Class: sheared ends.	
FEATURES	Location/Qualifiers	
SOURCE	1..796 /organism="Zea mays" /mol_type="genomic DNA" /strain="B73" /db_xref="taxon:4577" /clone_1fb="ZM.BT0566W14" /clone_1lb="ZM.0.6.1.0 KB" /note="Vector: pCR4-TOP0; Site 1: EcoRI; 0.6-1.0 kb high cot selected genomic DNA library"	
ORIGIN		
Query Match	12.8%; Score 114.4; DB 9; Length 796;	
Best Local Similarity	62.5%; Pred. No. 3.7e-21;	
Matches 365; Conservative 0; Mismatches 171; Indels 48; Gaps 10;		
Oy	318 GGATTGGGTGGAAGA---AATGCTCCCTTGAGCTTGTAACATGAAAGTAGTGAG	374
Dd	785 GTATTGGTTAAGAACATCAACAATTCCTCTCTGTCGCAAGAAACGSGTAG	726
Oy	375 TCATGAGTCACACTGATCCGATCTGATATATATAGCCAATGCTCACACCATTC	434
Dd	725 TCCATGCCGAGATCATCTCATCTGATATACATG-CTTACAGCTCACAAG--ACATTC	670
Oy	435 AAACAACCCCATCATATCATCAACAAGTTGTTTCATGAAAAACAATAAGTAGAG	494
Dd	669 AAAACAATC---AATATGCATTTACAAAAGTCGTTTCATGAAAAATPAAA---TAGGCCG	617
Oy	495 GAGGGGACATATATCTCTTGAGCGGCTAAAGTAATTTCAAGACATATATCAACT	554
Dd	616 GACAGGACAAAATTCCTTG---ACGTGTAAGTAATTTACACAAAAAAAAGCAAT	561
Oy	555 ATATCTAATTAATAGTTCGTTATATATACGACGATGATCAACAACCGTACTGTG	614
Dd	560 GTCAAGCTAAATCTAATTCGTTTTACGTAG-----ATCAACAACCTGAG	516
Oy	615 AAAGGCAACAAAATGAGCCAGCCAAAATGACAGATGAATCATATGATGAGAAAGTAC	674
Dd	515 AAGGCAACAAAATCGAGCCAGCCAGAAATACAGATGATTCACAGTGA-----AC	466
Oy	675 ACTGGGCTTGCTACATAAGTAAGTATGATGATCAATTAATTTGGCAAGAACGCTGAA	734
Dd	465 CATGACGCTGTAAGTAAGAGAGTGAAGATCATATCATTTGGCAAGAAACCTGAG	406
Oy	735 GCTACACAGCCGTGCTAGTAGCACAGAAACAAGAACTGTG---CTAATGAACT	790
Dd	405 CTGCTTACAGCCGCTCTCGTGGCATTAAGAACACAAAGAAATGTGTTAATTAATCAACT	346
Oy	791 ATAAATAACCTAAGTAGTATGACTTTCACATCACACATACCATATCTTCACTGA	850
Dd	345 ATAATAAGGCTCGATCCGTGTGACATCTTCATCACACACA-CTGGGCTTTCAGACCA	287

```

Oy      851   TTACCTTCTATCTACTCAAGAGCAGACAAGAATCCAGACC 894
          ||| | | | | | | | | | | | | | | | | | | | |
Db      286   TTACCTTATCTACTCCAGAGCCGACGAAGAACCCTGATCACACC 243

RESULT 4
CG024394                      896 bp    DNA        linear    GSS 19-AUG-2003
LOCUS       CG024394
DEFINITION  ZMMBc0561113f ZMMBc Zea mays genomic clone ZMMBc0561113 5',
ACCESSION   CG024394
VERSION     CG024394.1  GI:33896559
KEYWORDS    GSS.
SOURCE      Zea mays
ORGANISM    Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 896)
Bharti,A.K., Young,S., Kavchok,S., Keiser,G., Bronzino,A.C.,
Kozard,K., Fuks,G., Yu,Y., Ming,R. and Messing,J.
Sequencing of the maize genome at PGIR (2003b)
Unpublished (2003)
Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: Bharti@waksman.rutgers.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 434.
Location/Qualifiers
    1..896
        /organism="Zea mays"
        /mol_type="genomic DNA"
        /cultivar="B73"
        /db_xref="taxon:4577"
        /clone="ZMMBc0561113"
        /lab_host="E.coli DH10B"
        /clone_id="ZMMBc"
        /note="Vector: pYARBAC1.3; Site_1: BamHI; Site_2: BamHI"

ORIGIN
Query Match               11.7%; Score 105; DB 9; Length 896;
Best Local Similarity 71.3%; Pred.No.1.8e-18;
Matches 186; Conservative 0; Mismatches 60; Indels 15; Gaps 3;

Oy      608   ACCTGTAAAGGGCAACAATA-TGAGCAGCGAATAATGCAGATTCATTGATGAC 666
          ||| | | | | | | | | | | | | | | | | | | | |
Db      162   ACCGTGTAAAGGCAACAATACTGAGCCAGACGAAGTAGCATGATTTCCAGATGA----- 217
          ||| | | | | | | | | | | | | | | | | | | | |

Oy      667   GAACGTACACTCGGCTTGCTACATAAAGTAATGATGATCATATAATTTGGCAAGAA 726
          ||| | | | | | | | | | | | | | | | | | | | |
Db      218   -----ACATATCGACGTGCTACGTAAGGAAGAGGAGCGATCATATACATTTGGCAAGAA 271
          ||| | | | | | | | | | | | | | | | | | | | |

Oy      727   CCGTAAAAGCTACACAGCCGCTGCTAGTAGCACAGAACCAAGAACTGTG---CTAA 782
          ||| | | | | | | | | | | | | | | | | | | | |
Db      272   CCAATGAAGCTGCCACACAGCCGCTCGGTGCAATGAACCAATATATTGTGTTAATTA 331
          ||| | | | | | | | | | | | | | | | | | | | |

Oy      783   TCGAAGCTATAAATTAACCTAGTATGGCTATGCACTTCATCATCACACCTACCATATCT 842
          ||| | | | | | | | | | | | | | | | | | | | |
Db      332   TCAAAGCTATAAATTAAGCTGCGATGCGCTGTGCACTTCTCATATCACCAACATGCGGCTT 391
          ||| | | | | | | | | | | | | | | | | | | | |

Oy      843   TCACTATTATTACCTTCTCTA 863
          ||| | | | | | | | | | | | | | | | | | |
Db      392   TATATCTATTATCTTTATCTA 412
          ||| | | | | | | | | | | | | | | | | | |

```

LOCUS	CC159983	568 bp	DNA	linear	GSS 29-APR-2003
DEFINITION	ig06a11.g1 WGS-ZmaySF (Dhsa methyl1 filtered) Zea mays genomic clone				
ACCESSION	ig06a11, genomic survey sequence.				
VERSION	CC159983				
KEYWORDS	CC159983.1	GI:30184761			
SOURCE	GSS.				
ORGANISM	Zea mays				
AUTHORS	Zea mays				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.				
JOURNAL	1 (bases 1 to 568)				
COMMENT	Rabinowicz, P.D., O'Shaughnessy, A.L., Ballja, V., Dedhia, N., Katerzburger, F., King, L., Miller, B., Muller, S., Nascimeto, L., Zuber, V., McCormick, W.R., and Martensen, R.A. Genomic shotgun sequences from Zea mays (methyl1-filtered) Unpublished (2002)				
	Contact: W. Richard McCormick				
	Lila Annenberg Hazen Genome Sequencing Center				
	Cold Spring Harbor Laboratory				
	PO Box 100, Cold Spring Harbor, NY 11724, USA				
	Tel: 516 367 8884				
	Fax: 516 367 8874				
	Email: mccormick@cshl.org				
	Plate: ig06 row: a column: 11				
	Seq primer: -21M3UnivRev				
	Class: shotgun				
	High quality sequence stop: 568.				
FEATURES	Location/Qualifiers				
source	1..568				
	/organism="Zea mays"				
	/mol_type="genomic DNA"				
	/cultivar="B73"				
	/db_xref="taxon:4577"				
	/clone="ig06a11"				
	/lab_host="DH5a"				
	/clone_11b="WGS-ZmaySF (Dhsa methyl1 filtered)"				
	/note="Organ: Immature ears; Site_1: Xba I; Site_2: Xba I				
	The vector was digested with XbaI and one nucleotide was				
	added by fill in in the recessive 3' end. The genomic DNA				
	was nebulized, end repaired, adaptor ligated and size				
	fractionated using sephadex. The resulting fragments were				
	between 0.8 and 3 kb and were cloned into the vector (x/y				
	reads in M13mp19, .b/g reads in pUC19). The same ligation				
	was transformed into DH5a."				
ORIGIN					
Query Match	11.5%; Score 103.2; DB 8; Length 568;				
Best Local Similarity	69.5%; Pred. No. 5.2e-18;				
Matches 203; Conservative	0; Mismatches 73; Indels 16; Gaps 4				
0Y	608	ACCTGTGAAGGCAAA--TGACCACGCAAAATGCAATGATCATATGATGAC	666		
Db	16	ACCTTAGAGGCAAAACTGACCCACGCAAGTACAGATATTCAGATATA----	71		
0Y	667	GAACTGACCTGCGCTTGTCTACATTAAGTAATGATGACTTAATATTGGCAAGAA	726		
Db	72	-----ACCATGAGCGTGTCTAGTAAAGAGAGTGAAGTCAATATACATTTGGCAAGAA	125		
0Y	727	CCGTGAAGCTACACAGCCGTGCTGAGTAGCAACAGAACAGAAACGTG-----CTTA	782		
Db	126	CCATTAAGCTGCTACAGCGCTCTGGTGGCAATTAAGAACACAGAAATGTGTTAATTAA	185		
0Y	783	TCGAAGCTAATAATACCTTAGTATGCTATGCTATGCTATGCTATGCTATGCTATGCT	842		
Db	186	TCAAAGCTAATAATACGCTGCGATGCGCTGTGCTATCTTCATCAACACCA--CTGGGTCT	244		
0Y	843	TCAGTCTATTATCTTCTCTATCTATCTCCAGAGACACAGAAAGATGACACC	894		
Db	245	TCAGACCAATTACTTATCTATCTCCAGAGCGCAGAAAGAACCGATGACACC	296		
RESULT	6				

LOCUS	CG324647	757 bp	DNA	linear	GSS 26-AUG-2003
DEFINITION	OG2AT322TH_ZM_0.7_1.5_KB_Zea mays genomic clone ZMMBma0747F16,				
ACCESSION	CG324647				
VERSION	CG324647.1	GI:34241913			
KEYWORDS	GSS.				
SOURCE					
ORGANISM	Zea mays				
REFERENCE	Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.				
AUTHORS	1 (bases 1 to 757)				
TITLE	WhiteJaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T., Renick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunez,A., Robbins,D. and Lakey,N.				
JOURNAL	Consortium for Maize Genomics				
COMMENT	Unpublished (2002)				
	Other GSSs: OG2AT32TV				
	Contact: Cathy WhiteJaw				
	TIGR				
	9712 Medical Center Drive, Rockville, MD 20850, USA				
	Tel: 301-838-5843				
	Fax: 301-838-0208				
	Email: whiteJaw@tigr.org				
	Seq primer: TR				
	Class: sheared ends.				
FEATURES	Location/Qualifiers				
source	1..757				
	/organism="Zea mays"				
	/mol_type="genomic DNA"				
	/strain="873"				
	/db_xref="taxon:4577"				
	/clone="ZMMBma0747F16"				
	/clone_id="ZM_0.7_1.5_KB"				
	/note="Vector: pBSCSK-; Site 1: HincII; 0.7-1.5 kb				
	methylation filtered genomic DNA library"				
ORIGIN					
Query Match	9.1%; Score 81.8; DB 9; Length 757;				
Best Local Similarity	68.2%; Pred. No. 7e-12;				
Matches 144; Conservative 0; Mismatches 62; Indels 5; Gaps 2;					
Qy	688 CATAAAGCATGATGATGATCTATAATTTTGGCAAGAAACCGTAAAGCTACACAGCGCT 747				
Db	1 CGTAAAGAGATGACGAGCTCATATACATTTTGGCAAGAAACCATAGAGCTGCTACAGCG 60				
Qy	748 CGTCAGTAGCACAGGACACAAAGAACTGTG----CTAATCGAGCTATAATTAACCTTA 803				
Db	61 TCTCGGTGGCATTAAGAACACAAAGAAATTGTGTATTAATTAATTAAGCTTAACGCTC 120				
Qy	804 GTATGCCATATGCACTTCTCCATCAACCACTACCAATATCTAGTCTATTTTACCTTCTCTA 863				
Db	121 GGATCCCTGTGCACTTCTCCATCAACCACTA--CTGGGCTTTCAGACATTAAGCTTATCTTA 179				
Qy	864 TCTACTCCAGAGACACAAAGATGACAC 894				
Db	180 CTCACAGCGCAGAGAAACCCGATCGACACC 210				
RESULT 7					
AZ535206	AZ535206	832 bp	DNA	linear	GSS 03-NOV-2000
LOCUS	ENTQ017TF Entamoeba histolytica sheared DNA Entamoeba histolytica				
DEFINITION	genomic, genomic survey sequence.				
ACCESSION	AZ535206				
VERSION	AZ535206.1	GI:11092151			
KEYWORDS	GSS.				
SOURCE	Entamoeba histolytica				
ORGANISM	Entamoeba histolytica				
REFERENCE	Eukaryota; Entamebidae; Entamoeba.				
AUTHORS	1 (bases 1 to 832)				
	Loftus,B., Van Aken,S. and Fraser,C.				

TITLE
Determination of clone end sequences from Entamoeba histolytica
JOURNAL
HM1:IMSS sheared DNA library
COMMENT
Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: b.loftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library
Seq primer: M13-Forward
Class: shotgun
High quality sequence start: 33
High quality sequence stop: 814.
Location/Qualifiers

FEATURES

source

1. .832
/organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="HM1:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOSt; Site 1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."

ORIGIN

Query Match

5.6%; Score 49.8; DB 8; Length 832;

Best Local Similarity 46.2%; Pred. No. 0.0092;

Matches 200; Conservative 0; Mismatches 232; Indels 1; Gaps 1;

396 TCTGATATATATGCGCAATAGCTCACACGACAACTTACAAACCCCATATCATAT 455
301 TATTAAACATTTTAAATATAAATACTAAACAAATATCTCAATGAAATATTTAAT 360
456 CACAAAGTTGTTTCATGAAAAAACAATAAGTAGAGGGGACAAATATCTTGGCT 515
361 AAATATTTAATTTGAAAAATGAAATTAATCAATAAATTAAGAAATATGACATTAAT 420
516 TGACGCGTAAAGTAATTTACAAAGCCATATATCAACTATATCTAATTAATTAAGTTGCT 575
421 TGTGAAGATTAACAATGATTAATATCCATATATCATGAAATTAATTAATTAATTA 480
576 TATATATACGACATGATCA-TCAACAACCGTACTGTGAAGGCAACAAATGAGCCA 634
481 ACTATTCATACAAATTTCAATTAATTAATCAATATATATATTAATTAATTAATTA 540
635 CGCAAAATGCGAATGAAATCATATGATGACGAAGTCACTGGGCTTGTACATAAAG 694
541 TGAATAATTAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 600
695 TGAATGATGATCAATATATTTGGCAAGAAACCGTGAAGCTACACAGCGTGTGCT 754
601 ACATTCATTAAGAAATTAACAATAAGTAATTAAGTAAGTAAGTAAGTAAGTAAG 660
755 AGCAGAGAACACAGAAATCTGCTATATGAGCTATTAATTAATTAATTAATTAATG 814
661 AATTAAGAAATTAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATG 720
815 CACTTCTCATCA 827
721 ATGAATTCATTA 733

RESULT 8
BH158294/c 862 bp DNA linear GSS 24-SEP-2001
LOCUS
DEFINITION
ENTRI94TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
genomic, genomic survey sequence.

ACCESSION
BH158294
VERSION
BH158294.1 GI:15731732
KEYWORDS
SOURCE
ORGANISM
Entamoeba histolytica
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.

REFERENCE
1 (bases 1 to 862)
Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library (2001)
Unpublished (2001)

JOURNAL

Contact: Brendan J Loftus

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: b.loftus@tigr.org

Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library
Seq primer: M13-Forward
Class: shotgun

High quality sequence start: 15
High quality sequence stop: 855.
Location/Qualifiers

FEATURES

source

1. .862
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/strain="HM1:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOSt; Site 1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."

ORIGIN

Query Match

5.6%; Score 49.8; DB 8; Length 862;

Best Local Similarity 46.2%; Pred. No. 0.0093;

Matches 200; Conservative 0; Mismatches 232; Indels 1; Gaps 1;

396 TCTGATATATATGCGCAATAGCTCACACGACAACTTACAAACCCCATATCATAT 455
651 TATTAAACATTTTAAATATAAATACTAAACAAATATCTCAATGAAATATTTAAT 592
456 CACAAAGTTGTTTCATGAAAAAACAATAAGTAGAGGGGACAAATATCTTGGCT 515
591 AAATATTTAATTTGAAAAATGAAATTAATCAATTAATTAAGAAATATGAAACATTAAT 532
516 TGACGCGTAAAGTAATTTACAAAGCCATATATCAACTATATCTAATTAATTAAGTTGCT 575
531 TGTGAAGATTAACAATGATTAATATCCATATATCAATTAATTAATTAATTAATTA 472
576 TATATATACGACATGATCA-TCAACAACCGTACTGTGAAGGCAACAAATGAGCCA 634
471 ACTATTCATACAAATTTCAATTAATTAATCAATATGATTAATTAATTAATTAATTA 412

QY 635 CGCAAAATGCGAATGATTCATATGATGACGAAACGACAGCTGGGCTGTCTACATTAAG 694
 Db 411 TGAATAATGAAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 352
 QY 695 TGAATGATGATCATAATATTTTGGCAAGAAACCGTGAAGCTACAGACCGCTGCTAGT 754
 Db 351 ACATTCATTAAGATTAACAATAAAGATAAATAAGAAAGAAATTAAGTGAATTAAGA 292
 QY 755 AGCAGAGAACACAGAACTGCTCTAATCGAAGCTTAATTAACCTAGTATGCTATG 814
 Db 291 AATTAAGAAATTAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATG 232
 QY 815 CACTTCCTCATCA 827
 Db 231 ATGAATTCATTA 219
 RESULT 9
 BH150191/c 889 bp DNA linear GSS 27-AUG-2001
 LOCUS ENT0527F Entamoeba histolytica Sheared DNA Entamoeba histolytica
 DEFINITION genomic, genomic survey sequence.
 ACCESSION BH150191
 VERSION BH150191.1 GI:15311513
 KEYWORDS GSS.
 SOURCE Entamoeba histolytica
 ORGANISM Entamoeba histolytica
 Eukaryota; Entamoebidae; Entamoeba.
 REFERENCE Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.
 1 (bases 1 to 889)
 AUTHORS Determination of clone end sequences from Entamoeba histolytica
 TITLE HMI:IMSS sheared DNA library (2001)
 JOURNAL Unpublished (2001)
 COMMENT Contact: Brendan J Loftus
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0208
 Fax: 301 838 3543
 Email: b1loftus@igr.org
 Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
 DNA library
 Class: shotgun
 Seq primer: M13-Forward
 High quality sequence start: 24
 High quality sequence stop: 797.
 Location/Qualifiers
 1. 889
 /organism="Entamoeba histolytica"
 /mol_type="genomic DNA"
 /strain="HMI:IMSS"
 /db_xref="taxon:5759"
 /clone_lib="Entamoeba histolytica Sheared DNA"
 /note="Vector: pHO31; Site 1: Bst I; Constructed at The
 Institute for Genomic Research (TIGR), Rockville, MD.
 Genomic DNA isolated from broth cultures of E. histolytica
 using a method described by Clark and Diamond (Clark,
 C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
 method for isolate identification. Exp. Parasitol.
 77:450.). The DNA was mechanically sheared to give a
 tight size distribution (~2 kb). The v + i method used for
 the library construction is described in detail in Smith,
 H.O. and Venter, J.C. (Making small insert libraries for
 whole genome shotgun sequencing projects. In Genome
 Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrel, Oxford University Press, 1999)."
 ORIGIN
 Query Match 5.6%; Score 49.8; DB 8; Length 889;
 Best Local Similarity 46.2%; Pred. No. 0.0094;
 Matches 200; Conservative 0; Mismatches 232; Indels 1; Gaps 1;
 QY 396 TCTGATATATATGCCAATAGCTCACAGACAATTACAAACACCCCATCTATACAT 455

Db 473 TATTAAACATTTTAAATATACTAAACAAACAAATACTTCAAATGAAATATTATATAT 414
 QY 456 CACAAAGTTGTTTCATGAAAAAACAATAGATGACGAGGGGACATTAATCTTGGT 515
 Db 413 AATATATTATATATGAAAAATGAATTAATTAATTAATTAATTAATTAATTAATTAAT 354
 QY 516 TGACCGGTAAAGGAATTTTCAAGCATATATCAACCTATATCTAATTAATTAAGTTCGT 575
 Db 353 TGTGAAGAAATTAACATGATGATTAATATATCAATATCAAGAAATTAATTAATTAATTA 294
 QY 576 TATATATACCGACGATGATCA-TCAACAACCGTACCTGTGAAAGGCAACAAATGAGCCA 634
 Db 293 ACTATTCATCAATTTTCATCTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 234
 QY 635 CGCAAAATGCGAATGATTCATATGATGACGAAACGCTACCTGGCTGTCTACATTAAG 694
 Db 233 TGAATAATGAAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 174
 QY 695 TGAATGATGATCATAATATTTTGGCAAGAAACCGTGAAGCTACACAGCCGCTGCTAGT 754
 Db 173 ACATTCATTAAGATTAACAATAAAGATTAATTAAGAAAGAAATTAAGTGAATTAAGA 114
 QY 755 AGCAGAGAACACAGAACTGCTCTAATCGAAGCTTAATTAACCTAGTATGCTATG 814
 Db 113 AATTAAGAAATTAAGAAACACAAATTAATTAATTAATTAATTAATTAATTAATTAATG 54
 QY 815 CACTTCCTCATCA 827
 Db 53 ATGAATTCATTA 41
 RESULT 10
 A2678898 917 bp DNA linear GSS 14-DEC-2000
 LOCUS ENTJ957F Entamoeba histolytica Sheared DNA Entamoeba histolytica
 DEFINITION genomic, genomic survey sequence.
 ACCESSION A2678898
 VERSION A2678898.1 GI:11816044
 KEYWORDS GSS.
 SOURCE Entamoeba histolytica
 ORGANISM Entamoeba histolytica
 Eukaryota; Entamoebidae; Entamoeba.
 REFERENCE Loftus, B., Van Aken, S. and Fraser, C.
 1 (bases 1 to 917)
 AUTHORS Determination of clone end sequences from Entamoeba histolytica
 TITLE HMI:IMSS sheared DNA library
 JOURNAL Unpublished (2000)
 COMMENT Contact: Brendan J Loftus
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0208
 Fax: 301 838 3543
 Email: b1loftus@igr.org
 Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
 DNA library
 Class: shotgun
 Seq primer: M13-Forward
 High quality sequence start: 23
 High quality sequence stop: 893.
 Location/Qualifiers
 1. 917
 /organism="Entamoeba histolytica"
 /mol_type="genomic DNA"
 /strain="HMI:IMSS"
 /db_xref="taxon:5759"
 /clone_lib="Entamoeba histolytica Sheared DNA"
 /note="Vector: pHO31; Site 1: Bst I; Constructed at The
 Institute for Genomic Research (TIGR), Rockville, MD.
 Genomic DNA isolated from broth cultures of E. histolytica
 using a method described by Clark and Diamond (Clark,
 C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a

method for isolate identification. Exp. Parasitol. 77(450). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Borell, Oxford University Press, 1999).

ORIGIN

Query Match 5.6%; Score 49.8; DB 8; Length 917;
Best Local Similarity 46.2%; Pred. No. 0.0094;
Matches 200; Conservative 0; Mismatches 232; Indels 1; Gaps 1;

QY 396 TCTGATATATATGCAAAATAGCTCAGACGACATTAACAAACCCCATATCATACAT 455
DB 384 TATTAACATTTTAAATATAAATAAACAACAAATACCTCAATGATATTTATATAT 443
QY 456 CACAAAGTTTGTTCATGAAAAAACAATAGTATGAGGAGGACATATCTTGTCT 515
DB 444 AATATATTTAATATGAAAAATGAAATTAATCAATTAATTAATGAAATATATAT 503
QY 516 TGACGCTAAAGTAAATTTTACAAAGCCATATATCACTATATCTAATTAATAGTTCT 575
DB 504 TGTCAAGAAATTAACAAATGATATATCAATATATCAATTAATTAATTAATTAATCA 563
QY 576 TATATATATGCGACGATGATCA-TGACAAACCGTACTGTGAAAGCAACAAATGAGCA 634
DB 564 ACTATTCATCAATTTTCATTTAATATATCAATATGATATTAATCACTTAATGAAATA 623
QY 635 CGCAAAATGCAATGATCATATGATGACGAACGTAACCTGCGTCTTACATTAAG 694
DB 624 TGAATAAATAAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 683
QY 695 TGAATGATGATCAATATATTTGGCAAGAAACCGTGAAGCTACACGCGTGTGACT 754
DB 684 ACAATCTTAAAGATTAACAAATTAAGATTAATTAAGAAATTAAGATTAAGATTAAG 743
QY 755 AGCAGACAGACACAAAGAACTGTCTATGACGATTAATTAATTAATTAATTAATTA 814
DB 744 AATTAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 803
QY 815 CACTTCTCATCA 827
DB 804 ATGAATTCATTA 816

RESULT 11
CNS006MN 693 bp DNA linear GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TERT3 end of BAC #
DEFINITION BACRI4H07 of RPI-98 library from Drosophila melanogaster (fruit
fly) genomic survey sequence.
ACCESSION AL065759
VERSION AL065759.1 GI:4944626
KEYWORDS Drosophila melanogaster (fruit fly)
SOURCE Drosophila melanogaster
ORGANISM Drosophila melanogaster (fruit fly)
REFERENCE 1 (bases 1 to 693)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage ;
BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osogawa and

Aaron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source 1..693
location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACRI4H07"
/clone_1db="RPI-98"
/note="end : TERT3"

ORIGIN

Query Match 5.5%; Score 49.6; DB 9; Length 693;
Best Local Similarity 32.9%; Pred. No. 0.01;
Matches 195; Conservative 73; Mismatches 324; Indels 0; Gaps 0;

QY 274 ATCCATCAACAATCCGACGACATCACAAAATTCGACGTCATGAGTGGTGAGAAAC 333
DB 14 ANNGAAAAATVAAABVDAANAAAAAAGAAAGAAATGACAAATATGATGAAATTA 73
QY 334 AATCGTCTCCTGTATGATCTGTATCAATGAGTATGAGTCACTGATGATCC 393
DB 74 AATTTTGAAGATGATGAGGTGAAAAAAMAAATTAATTAATTAATTAATTAATTTCC 133
QY 394 GATCTGATATATATGCAAAATAGCTCACACGACATTAACAAACCCCATATCTATAC 453
DB 134 ANTNTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 193
QY 454 ATCAAAAGTTTGTTCATGAAAAAACAATTAATTAATTAATTAATTAATTAATTAAT 513
DB 194 AATTAATTTTCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 253
QY 514 CTGACCGCTGAAGTGAATTTTCAAAAGCCATATATCAACCTATATTAATTAATTAAT 573
DB 254 ACMAACCCACACCCMCMCAAAACMAAAACMAAAACMAAAACMAAAACMAAAACMAAA 313
QY 574 GTTATATATATGCGACGATGATCAACAACCGTACCTGTGAAGCAAAATGAGCC 633
DB 314 AMACAAACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 373
QY 634 ACGCAAAATGCAATGATTCATATGATGACGACGATGATGATGATGATGATGATGAT 693
DB 374 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 433
QY 694 GTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 753
DB 434 AATTAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 493
QY 754 TAGCAGACGACACAAAGAACTGTCTAATGCAAGCTATTAATTAATTAATTAATTA 813
DB 494 NCCMAAAKAAANAAABRMKMSBKSAAGMCCMGTAMMMCMCHMMAAAAVAVY 553
QY 814 GCATTTCTCATCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 865
DB 554 SCTSCBCCSCSYSTCYCCCTCGTMTMMCKMTCTVKTMYBGBYTKTC 605

RESULT 12
BHI6284 912 bp DNA linear GSS 24-SEP-2001
LOCUS BHI6284
DEFINITION ENTPF68TR Entamoeba histolytica sheared DNA Entamoeba histolytica
ACCESSION BHI6284
VERSION BHI6284.1 GI:15739722
KEYWORDS GSS.
Entamoeba histolytica

ORGANISM

Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.

REFERENCE

1 (bases 1 to 912)
Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.

AUTHORS

Determination of clone end sequences from Entamoeba histolytica
HML:IMSS sheared DNA library (2001)

JOURNAL

Unpublished (2001)

COMMENT

Contact: Brendan J Loftus

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 3543

Email: b.loftus@tigr.org

Clones are derived from the Entamoeba histolytica HML:IMSS sheared

DNA library

Seq primer: M13-Reverse

Class: shotgun

High quality sequence start: 10

High quality sequence stop: 739.

FEATURES

source

1..912

/organism="Entamoeba histolytica"

/mol_type="genomic DNA"

/strain="HML:IMSS"

/db_xref="taxon:5759"

/clone_lib="Entamoeba histolytica Sheared DNA"

/note="vector: pHOSt1, Site 1: Bat I; Constructed at The

Institute for Genomic Research (TIGR), Rockville, MD.

Genomic DNA isolated from broth cultures of E. histolytica

using a method described by Clark and Diamond (Clark,

C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a

method for isolate identification. Exp. Parasitol.

77:450.). The DNA was mechanically sheared to give a

light size distribution (~2 kb). The v + i method used for

the library construction is described in detail in Smith,

H.O. and Venter, J.C. (Making small insert libraries for

whole genome shotgun sequencing projects. In Genome

Sequencing: A Practical Approach, eds. M. Vaubin and B.

Barell, Oxford University Press, 1999)."

ORIGIN

Query Match 5.5%; Score 49.6; DB 8; Length 912;

Best Local Similarity 46.4%; Pred. No. 0.011;

Matches 195; Conservative 0; Mismatches 224; Indels 1; Gaps 1;

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Oy 396 TCTGATATATATGCCAATAGCTCACGACACATTACAAACCCCACTATACAT 455
Db 251 TATTAACATTTTATATATACTAAACAAACAAATACCTTCAATGAAATATTAAT 310
Oy 456 CACAAAGTTTTCATGAAAAACAATTAAGTAGCGAGGGGACAAATATCCTTGCT 515
Db 311 AAATATTTAATATGAAAAATGAAATTAATACATTAATAAGAAAATGTGAACATTAAT 370
Oy 516 TGAGCGCTAAAGTGAATTTACAAAGCCATATATCAATATCTAATTAATTAAGTTGCT 575
Db 371 TGTGAAGAAATAAACATGATATATCCATATATCTGAAATTAATTAATTAATTAAT 430
Oy 576 TATATATATGCAACGATATCA-TCACAAACCGTACCTGTGAAGGCAACAAATGAGCCA 634
Db 431 ACTATTCATACATTTTCATCATTAATAATATCAATATATATAAATTAATTAATTA 490
Oy 635 CGCAAAATGCGAATGGAATCCATATGATGACGAACGTAACCTGGCTTGCTACATAAG 694
Db 491 TGAATAATTAAGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 550
Oy 695 TGAATGATGATGATTAATTTTGGCAAGAAACCTGAAAGCTACACAGCGTCTGCTAGT 754
Db 551 ACAATCATTAAGAAATTAACAATTAAGAAATTAAGAAAGGAAATTAAGGAAATTAAGA 610
Oy 755 AGCAGGAAACAAAGAACTGTGCTAATCGAAGCTATTAATTAATCCATGATGCTTATG 814
Db 611 AATTAAGAAATTAAGAAACCAATTAATTAATTAATTAATTAATTAATTAATTAATG 670

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RESULT 13

LOCUS

CD384866

DEFINITION

CD384866

ACCESSION

CD384866

VERSION

CD384866.1

KEYWORDS

EST.

ORIGIN

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 1067)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgabs-remail.nih.gov

Tissue Procurement: Dr. Jamie Thompson, University of WI

CDNA Library Preparation: Gina Zaibrow-Hayes

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LMNL at:

http://image.llnl.gov

Plate: NDKW5 row: 1 column: 01

High quality sequence start: 27

High quality sequence stop: 320.

Location/Qualifiers

1..1067

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue_type="embryonic trophoblasts, made from WA01 stem

cells"

/lab_host="DH10B TONa"

/clone_lib="NIH-MGC 173"

/note="vector: pDONR201; Site 1: attP2; Site 2: attP1;

LIBR PRIMING - oligo dt; METHOD - full-length enriched;

LIBR PROVIDER - Bradfield"

ORIGIN

Query Match 5.2%; Score 46.8; DB 6; Length 1067;

Best Local Similarity 31.7%; Pred. No. 0.07;

Matches 153; Conservative 0; Mismatches 329; Indels 0; Gaps 0;

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Oy 322 TGGGTCGAAACAATCGTCTCCTTGATGCTGTGACAAATGAGATGATGATCATGAG 381
Db 361 TCGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 420
Oy 382 TCACATGATCCGATCGATATATATATGCAATAGCTCACGACCAACATTACAAACAC 441
Db 421 AAAAAAANNNGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 480
Oy 442 CCCATCTATATCATCAAAAGTTGTTTCATGAAAAAACAATTAAGTAGAGAGAGGA 501
Db 481 AAAAAAANNNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 540
Oy 502 CAATATATCCTTGCTGACGCGTAAGTAATTACAAAGCCATATATCAACTTATCTA 561
Db 541 AAAAAAANNNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 600
Oy 562 ATTAATAAGTTCGTTATATATATACGACATGATCATCAACACCGTACCTGTAAGCA 621
Db 601 AAAAAAANNNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 660
Oy 622 ACAAATGAGCGACGCAAAATGCAAGATGAATCATATATGAGCAACGATGCTGGC 681
Db 661 AAAAAAANNNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNAANNA 720

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QY 682 TTGCTACATAAAGTAAATGATGATCATTAATTTGGCAGAAACCGTGAAGCTACAC 741
 Db 721 NNN 780
 QY 742 AGCGCTGCTGAGTACAGACAGAACTGTGCTAATCGAAGCTATTAATTAACCC 801
 Db 781 NNN 840
 QY 802 TA 803
 Db 841 NA 842

RESULT 14
 A1809613/c 462 bp mRNA linear EST 19-DEC-1999
 LOCUS w31d09.x1 Soares_NFL_T GBC_S1 Homo sapiens cDNA clone
 DEFINITION IMAGE:2357201.3', mRNA sequence.
 ACCESSION A1809613
 VERSION A1809613.1 GI:5396179
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 462)
 AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov.
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 1160 Std Error: 0.00
 Seq primer: -40UP from G1pco
 High quality sequence stop: 444.
 Location/Qualifiers
 1..462
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /cclone="IMAGE:2357201"
 /lab_host="DH10B"
 /cclone_id="Soares_NFL_T_GBC_S1"
 /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
 a modified polylinker; Site 1: Not I; Site 2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung NBHL19W, testis NHT, and B-cell
 NCI-CCAP GCB1) were mixed, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 I.M.A.G.E. clones 297480-302087, 682632-687239,
 726408-728711, and 729096-731399. Subtraction by Bento
 Soares and M. Fatima Bonaldo."

ORIGIN
 Query Match 5.1%; Score 45.6; DB 1; Length 462;
 Best Local Similarity 48.8%; Pred. No. 0.13; Indels 0; Gaps 0;
 Matches 123; Conservative 0; Mismatches 129; Indels 0; Gaps 0;
 QY 414 TAGCTCAGCAGCAACATTAACAACCCCATCTACTACATCAACAAGTTGTTGATG 473
 Db 418 TAGCTGCTGATTTATTTAAACAAAGATACAACTCAAGAAATTAATCTG 359
 QY 474 AAAAAAACAATAGTATGACGAGGAGCAATTAATCTTGTGACCGGTAAAGTAAT 533
 Db 358 AAAATAGTTGACGATCTCAACAGGGGAAATGATACATGATATGATATACAGATA 299
 QY 534 TACAAAGCATATATCAACCTATATTAATTAAGTTCGTTATATATACGACGATGA 593

Db 298 CACGATTAATATATATATACAAATATGATAGAAAGTAATTTTATTTAGCATATATGA 239
 QY 594 TCATCAACAACCGTACTGTGAAGGCAACAAATGACGACGAAATGCAAGTGA 653
 Db 238 AAAAAGCTAATACTACTGCTGAAGAAATTAACAGTTTCAGGGAAACAAACATTAATAA 179
 QY 654 TCCATATGATGA 665
 Db 178 CAAAAGGTATGA 167

RESULT 15
 CD388513 949 bp mRNA linear EST 30-MAY-2003
 LOCUS AGENCOURT_14346106 NIH_MGC_173 Homo sapiens cDNA 5', mRNA sequence.
 DEFINITION CD388513
 ACCESSION CD388513.1 GI:31226753
 VERSION CD388513.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 949)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Dr. Jamie Thompson, University of WI
 cDNA Library Preparation: Gina Zastrow-Hayes
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: NDKM68 row: e column: 06
 High quality sequence stop: 519.
 Location/Qualifiers
 1..949
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic trophoblasts, made from WA01 stem
 cells"
 /lab_host="DH10B Tona"
 /cclone_id="NIH_MGC_173"
 /note="Vector: pDONR201; Site 1: attP2; Site 2: attP1;
 LTR PRIMER - oligo dT; METHOD - full-length enriched;
 LIBR PROVIDER - Bradfield"

ORIGIN
 Query Match 5.1%; Score 45.4; DB 6; Length 949;
 Best Local Similarity 31.1%; Pred. No. 0.17; Indels 0; Gaps 0;
 Matches 133; Conservative 0; Mismatches 295; Indels 0; Gaps 0;
 QY 371 TGAATCATGATCACTATCGATCTGATATATATGCAATAGCTACAGACAGACA 430
 Db 462 TAAGTCTTTGTAATTTGGCTTTCTTAATTAACCACTTAGTTGATCAANAAA 521
 QY 431 TTACAAACAACCCCATCTACTATACATCAACAAGTTGTTTCATGAAAAACAATAGTAT 490
 Db 522 AAAAAAANNN 581
 QY 491 GCAGAGGAGCAATTAATCTTGTGACCGGTAAAGTGAATTTCAACACCATATATCA 550
 Db 582 AAAAAAANNN 641
 QY 551 ACCTATATCTAATTAATTAAGTTCGTTATATATGACGATGATCAACAACCGTACC 610

Db 642 NNNNNNNNNNNNNNNNNATTTTTTTAAAAAANNNNNNNAAAAAANNNNNNN 701
Qy 611 TGTGAAAGGCAACAAATGAGCCAGCAAAATGCAGATGATCCATATGATGACGAC 670
Db 702 NNNNNNNNNNNNNNNNNAAAAAANNNNNNNAAAAAANNNNNNN 761
Qy 671 GTACACTCGGCTTGCTACATAAAGTGAATGATGATCATTAATTTGGCAAGAAACCGT 730
Db 762 AANNNNNNNNNNNNNNNNNAAAAAANNNNNNNAAAAAANNNNNNN 821
Qy 731 GAAAGCTACACAGCCGTCGTAGTACACAGAAACACAGAACTGTCTAATCGAACT 790
Db 822 AAAAAAAAAAAAAAAAAATTANNNNNNNNNAAAAAANNNNNNNNNNNNA 881
Qy 791 ATAAATTA 798
Db 882 AAAAAAAAA 889

Search completed: September 24, 2005, 17:02:51
Job time : 3152 secs


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Oy 270 TGTATTCATACAAACAATCCGAGAAACATCAAAATTGGACGTCATAGC-AATGGGCTCA 328
Db 6783 TTGTATCTCTTAACAACATCAACAGAACATCAACCAAAATTGGACAGCTAAAGGATATGGGTAA 6724
Oy 329 GAAACAAATCGTCTCTCTTGTAGCTTGTACAAATGAAGTATGGTATGATGATGACACT 388
Db 6723 GAAACAAATCAAAACAATCTCTCTCTGTGTGCAAAAGAAACACGGTATGATG-CCGAGATC 6655
Oy 389 GATCCGATCTGATATATATATGCCAAATAGCTCACACGACAACTTATCAAAACAACCCCATAC 448
Db 6664 ATATCATCTGATATATACATG-CTTACACTCAAGA---ACATTCAAAACAACCTC---AT 6612
Oy 449 TATACATCAAAAGTTGTTTCATGAAAAAAACAAATAGTATGACGAGGGGACAAATAT 508
Db 6611 ATTGCATTACAAAGATCGTTTCATGAAAAATAAA---TAGCCGCGACAGGACAAAAT 6556
Oy 509 CTTGCTTGACGCGTAAAGTAAATTTAGCAAGCCATATATCAACCTATATCTAATTAATA 568
Db 6555 C---CTTGACGCTGTAAGTAAATTTACAA---CAAAAAAAGCCATATGTACAGCTAA 6503
Oy 569 AGTTGCTATATATATACGACGATATCATCAACAACCGTACTCTGTGAAGGCAACAAT 628
Db 6502 ATCTAATTCGTTTACGTATGATCAACAACCTGTGTA-----GAAAGCAACAAAAC 6455
Oy 629 GAGCCACGCCAAAAATGSCAGAAATGAATTCATATGATGACGAAAGTACACTCGGCTGTCTAC 688
Db 6453 GAGCCACGCCAAGAAAGTACAGAAATGATTTCCAGATGA-----ACATCAACGCTGTCTAC 6400
Oy 689 ATAAAGTAATGATGATGATCATTAATATTTTGGCAGAAACCGTGAAAGCTACACAGCCGT 748
Db 6403 GTAAAGAAAGAGTACAGATCATATATTTGGCAGAAACCATGAAGCTGTGCTACAGCCGT 6344
Oy 749 GTCGATGACACAGAAACAAGAACTGTG---CTAATCGAGGTATTAATTAACCCCTAG 804
Db 6343 CTCGGTGCATPAAGAACACAAGAAATTTGTATTAATTAACAAGCTAATTAATTAACGCTCG 6284
Oy 805 TATGCGTATGCACTTCTCCATCAGCACTAACCCATATCTTCAGTCTAATTTACCTTCTCTAT 864
Db 6283 CATGCTGTGCACTTCTCTCATACCAACCA-CTGGGCTTTCAGACACTT---AGCTTAT 6222
Oy 865 CTACTCCAGAGACACAGAAATGACACC 894
Db 6228 CTACTCCAGAGCGCAGAAACCCCGTACC 6199

RESULT 2
US-10-228-063-12
; Sequence 12, Application US/10228063
; Publication No. US20030135885A1
; GENERAL INFORMATION:
; APPLICANT: Lanahan, Mike
; TITLE OF INVENTION: Self-processing Plants and Plant Parts
; FILE REFERENCE: 109846,317
; CURRENT APPLICATION NUMBER: US/10/228,063
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Zea mays
US-10-228-063-12

```

Query Match	16.0%	Score 142.6	DB 15	Length 673
Best Local Similarity	65.3%	Pred. No. 5, 2e-30		
Matches	430	Conservative	0	Mismatches 179; Indels 50; Gaps 13
OY	214	CCTAAGGATGATGAGAAATTCGGAACGAC-----CATTCGCATCTAGACGCTGTGAATTGG	269	
	27	CCTAAGGATGATGAGAAACGAAACCAACCATTCGATTTGGCATTTAAAGCTCCAAAGAAATTTG	86	
OY	270	TGTTATTCATACAAACAACTTCGAGAAATCATCAAAAATTTCACGTCGAATGG-ATTGGAGTCA	328	

Db	87	TTGATTCCTTAACTCAACAGAACTCAACCAAAATTGCAAGTCAAGGATATTGGGTAA	14
Qy	329	GAACAACATGCTCTCCTTGAAGCTTGACATGAAGTAGTGSTAGATCA	38
Db	147	GAACAACATCAACAAATCCCTCTCTGTGTGCACAAAGAACCGGTGATCATG--CCGAGATC	20
Qy	389	GATCCGATCGATATATATATGCCCACAAATAGCTCACAGACAACATTTCAACCAACCCCATTC	44
Db	206	ATACTCATCTGATATATCATG--CTTACAGCTCACAG--ACATTCAACCAACTC---AT	25
Qy	449	TATACATCACAAAGTTTGTTTTCATGAAAAACAAATAGTATGACGAGGGGACATAAT	50
Db	259	ATTGCATTATCAAAAGATCGTTTTCATGAAAAATATAA---TAGCGCGGACAGGACAAAAT	31
Qy	509	CTTGTCTTGAACGGTAAAGTGAAATTTACAAAGCCATATATCAACCTATATCTAATTAATA	56
Db	315	C----CTTGAACGGTAAAGTAAATTTACAA---CAAAAAAAGCCATATGTCAAGCTTA	36
Qy	569	AGTTCGTTATATATATACGACATGATCATCAACAAACCGTACCTGTGAAAGGCAACAAAT	62
Db	368	ATCTAATTCGTTTATCGTAGATCAACAACCTGTA-----GAAGGCAACAAACT	41
Qy	629	GAGCCACGCAAAAATGACAGATGATCAATATGATGACGACGTACACTCGCTTGCTAC	68
Db	417	GAGCCACGACGAAAGTACAGATGATATTCACAGATGA-----ACCATCGACGTCTAC	46
Qy	689	ATAAAGATATGATGAGTCATTAATATTTGGCAAGAAACCGTAAAGCTACACAGCCGC	74
Db	467	GTAAGAGAGTACGAGTCAATATCACTTTGGCAAGAAACCATGAAAGCTGCTACAGCCGT	52
Qy	749	GTCAGTAGCAACAGAACACAAAGAACTGTG---CTAATCGAAGCTATTAATAACCTTAG	80
Db	527	CTGGTGGCATATAGAACACAAAGAAATGTGTATTAATCAAGGCTATTAATAAGCTCG	58
Qy	805	TATGCCATATGCACTTCTCCATCAACCACTACACCATATCTTCACTATTAACCTTCTTA	863
Db	587	CATCCCTGTGCACCTTCTCCATCAACCA--CTGGGCTTTCAGACCATTAAGCTTTATCTA	644

```

RESULT 3
; Sequence 13, Application US/11/074522
; Publication No. US20050198712A1
; GENERAL INFORMATION:
; APPLICANT: Syngenta Participations AG
; APPLICANT: Betts, Scott
; APPLICANT: Skalla, Dale
; APPLICANT: Volrath, Sandra
; APPLICANT: Hendrickx, Koen
; TITLE OF INVENTION: Q-PROTEIN SEQUENCE AND PROMOTER
; FILE REFERENCE: 1392/22/2
; CURRENT APPLICATION NUMBER: US/11/074,522
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US 60/551,266
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 13
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(6)
; OTHER INFORMATION: 5' Hind III recognition sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (682)..(687)
; OTHER INFORMATION: 3' BamH I recognition sequence
US-11-074-522-13

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? PRIOR FILING DATE: 2003-11-07
? PRIOR APPLICATION NUMBER: 11/011,526
? PRIOR FILING DATE: 2004-12-14
? NUMBER OF SEQ ID NOS: 32
? SOFTWARE: FastSeq for Windows Version 4.0.
? SEQ ID NO 26
? LENGTH: 1510
? TYPE: DNA
? ORGANISM: Zea mays
? FEATURE:
? NAME/KEY: promoter
? LOCATION: (1)...(1510)
? OTHER INFORMATION: GZ-w64a promoter
US-11-063-325-26

```

Query Match	16.0%	Score 142.6;	DB 24;	Length 1510;
Best Local Similarity	65.3%	Pred. No. 7.9e-30;		
Matches 430; Conservative	0;	Mismatches 179;	Indels 50;	Gaps 13;

QY	214	CGTAAAGGATGAGGAATAACGGAACGAC----	CATTGGCATGTAGAGCTGATGAATTGG	269
Db	864	CCTTAAGGTGTGAGGAACACGAAACACCATG	CATTGGCATGTGAAGCTCCACAGATTTGG	923
QY	270	TGTTATCCATACACACACTCGCAGAAATCA	CAAAATTGGCACTGTCMAATGG--ATTGGGTCA	328
Db	924	TTGTATCCTTTAACAACTCACAGAACTCA	CAAAATTGGCACTGTCMAAGGATTTGGGTAA	983
QY	329	GAACAAATCGCTCTCCTTGTAGCTTGTAC	AATGAAGTGAATGGTGAATCATGATGACACT	388
Db	984	GAACAAATCAAAACAATCCTCTGTGTGTG	CAAGAAACAGGTGTGATGTC--CCGAGATC	1042
QY	389	GATCCGATCTGTATATATATGCGCAAT	TAGCTCACAGCAACATTACAAACAACCCATAC	448
Db	1043	ATATCATCTGTATATATACATG--CTTAC	AGCTCACAG--ACATTACAAACAACCTC--AT	1099
QY	449	TATACATCACAAAGTTTGTTCATGA	AAAAACAATTAAGTATGACGAGGGGACCAATAT	508
Db	1096	ATTGCATTACAAAGATCGTTTCATGA	AAAAATTTAAA--TAGGCGGACAGGACAAATAT	1151
QY	509	CCTTGCTTACGGCGTAAAGTGAATTTAC	AAAGCCATATATCAACTATATCTTAATTAATA	568
Db	1152	C----CTTGACGTGTAAAGTAATTTACAA--	CAAAAAAAGCCATATGTGCAAGCTTAA	1204
QY	569	AGTTGGTATATATACGACAGATGATCAT	CAACAACCGTACTGTGAAGGCAACAAATAT	628
Db	1205	ATCTAATTCGTTTTCGTATGATCAACAC	ACTGTGTA-----GAAGCAACAAACT	1255
QY	629	GAGCCAGCCAAAATGACAGATGAATTC	ATATGATGACGAACGTACACTCGGCTTTGTAC	688
Db	1254	GAGCCAGCCAGAGTACAGAAATGATTC	AGATGA-----ACCATCGACGTGTAC	1303
QY	689	ATTAAGTGAATGATGATGATCATTAAT	TGGCAAGAAACCGTGAAGACTACACAGCCGT	748
Db	1304	GTAAGAGAGTACACAGTCTATATACAT	TGGCAAGAAACCAATGAAGCTGTCTACAGCCGT	1363
QY	749	GTCACTAGCACAGAAACAAGAAACTGTG--	CTAATCGAAGCTATTAATTAACCTTAG	804
Db	1364	CTCGGTGGCATTAAGAACACAAAGAAAT	TGTGTTAATTAATCAAGCTATTAATTAACGCTCG	1422
QY	805	TATGCGTATGCACTTCTCATCAACACT	ATACCCATATCTTCAAGTCAATTTACTCTCTTA	863
Db	1424	CATGCGTGTGCACTTCTCATCAACACCA	CA--CTGGGCTTTCAGACCACTTAGCTTTATCTTA	1481

RESULT 6
US-11-074-522-18
; Sequence 18, Application US/11074522
; Publication No. US2005018712A1
; GENERAL INFORMATION:
; APPLICANT: Syngenta Participations AG
; APPLICANT: Batts, Scott
; APPLICANT: Skalla, Dale
; APPLICANT: Volrath, Sandra

```

: APPLICANT: Hendrickx, Koen
: TITLE OF INVENTION: O-PROTEIN SEQUENCE AND PROMOTER
: FILE REFERENCE: 1392/22/2
: CURRENT APPLICATION NUMBER: US/11/074,522
: CURRENT FILING DATE: 2005-03-08
: PRIOR APPLICATION NUMBER: US 60/551,286
: PRIOR FILING DATE: 2004-03-08
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 18
: LENGTH: 5290
: TYPE: DNA
: ORGANISM: Artificial
: FEATURE:
: OTHER INFORMATION: Artificial intermediate plasmid encoding gamma zein
: FEATURE:
: OTHER INFORMATION: promoter-gamma zein signal sequence-gala fusion
: NAME/KEY: misc feature
: LOCATION: (1)..(5290)
: OTHER INFORMATION: The sequence presented is of a circular molecule
: US-11-074-522-18

```

Query Match	16.0%	Score 142.6;	DB 24;	Length 5290;
Best Local Similarity	65.3%	Pred. No. 1.5e-29;		
Matches 430; Conservative	0;	Mismatches 179;	Indels 50;	Gaps 13;

QY	214	GTAAAGATGAGAGAAATACGAACGAC----	CATTGGCATGTAGAGCTGTATGAATTGG	269
Db	2908	CCTTAAGTGTGAGAGAACACGAAACACCAATGCATTGGCATGTAAAGCTCCAGAAATTTG		2966
QY	270	TGTTATCCATACCAACACTCGCAGAACATCAACAAATTCGACGTCMAATGG-ATTGGGTCA	328	
Db	2968	TTGTATCCTTAAACAATCACAAGAACATCAACCAAAATTGCACGTCGAAGGGTATTGGGTAA	3027	
QY	329	GAACCAATTCGTCTCTCTTGTAAGCTTGTACAAATGAAGTGTAGTGATGATCAATGACACT	388	
Db	3028	GAACCAATTCGAACAAATCTCTCTGTGTGCAAGAAACACCGTATGTCAT-CCGAGATC	3086	
QY	389	GATCCGATCTGATATATATATGCGCAATATAGCTCACACGACACATTACAAACAACCCCATAC	448	
Db	3087	ATACTCATCTATATATACATG-CTTACAGCTCACAG--ACATTACAAACAATC--AT	3139	
QY	449	TATACATCACAAAGTTGTTCATGAATAAAACAAATTAATGATGACGAGGGGACATATAT	508	
Db	3140	ATTGCATTACAAAGATCGTTTCATGAATAAAATATAAA--TAGCGCGGACAGACAAAAT	3195	
QY	509	CCTTGCTTGAAGCGCTAAAGTAATTTCAAGCCATATATCAACTATATCTAATTAATA	568	
Db	3196	C-----CTTGACGTGTAAAGTAATTTACAA--CAAAAAAAAAAGCATATGTCAAGCTAA	3248	
QY	569	AGTTGCTATATATATACGACCATATATCATCAACAACCGTACTGTCGAAGGCAACAAAT	628	
Db	3249	ATCTATATTCGTTTATCGTATGATCAACAACCTGTA-----GAAGGCAACAAACT	3297	
QY	629	GAGCCACGCCAAAAATGCAGATGAATTCATATGATGACGAACGTACACTCGGCTTGCTAC	688	
Db	3298	GAGCCACGCCAAGATACAGAAATGATTTCCAGATGA-----ACCATTCACCGTCTAC	3347	
QY	689	ATTAAGTAATGATGAGTCATTAATATTTTGGCAAGAAACGGTGAAGCTACACAGCCGTC	748	
Db	3348	GTAAAGAGTGAAGAGTCATATATCATTTTGGCAAGAAACATGAAGCTGCTTACAGCCGT	3407	
QY	749	GTCAGTGAACAGGAACAACAAGAAACTGTG----CTAATCGAAGCTATAAATTAACCTTAG	804	
Db	3408	CTCGGTGSCATTAAGAACACAAGAAATGTGTTAATTAATCAADAGTATAAATTAACGCTCG	3466	
QY	805	TATGCTTATGCACTTCTTCATCAACCACTAACCAATATCTTCACTATTATTAACCTTCTCTA	863	
Db	3468	CATGCTGTGCACTTCTTCATCACACACA-CTGGGCTTTCAGACCATTAGCTTATATCTA	3525	

RESULT 7
US-11-074-522-16

```
; Sequence 16, Application US/11074522
; Publication No. US20050198712A1
; GENERAL INFORMATION:
; APPLICANT: Syngenta Participations AG
; APPLICANT: Belts, Scott
; APPLICANT: Skalla, Dale
; APPLICANT: Voitrach, Sandra
; APPLICANT: Hendrickx, Koen
; TITLE OF INVENTION: O-PROTEIN SEQUENCE AND PROMOTER
; FILE REFERENCE: 1392/22/2
; CURRENT APPLICATION NUMBER: US/11/074,522
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US 60/551,286
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 5912
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial intermediate plasmid encoding gamma-zein-gala fusion
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)_(5912)
; OTHER INFORMATION: The sequence presented is of a circular molecule
US-11-074-522-16

Query Match      16.0%; Score 142.6; DB 24; Length 5912;
Best Local Similarity 65.3%; Pred. No. 1.6e-29;
Matches 430; Conservative 0; Mismatches 179; Indels 50; Gaps 13;

QY 214 CGTAAAGTGTAGGAAATACGAAACGAC---CATGGCATGTAGAGCTGTATGAATTGG 269
DB 2309 CCTAAAGTGTAGGAAACAGAAACAACCATGATGGCATGTAAAGCTCCAAAGATTGG 2968
QY 270 TGTATCCATACCAACAACCTGCCAGACATCAACAATTGCGACGTCAATGG-ATTGGGTCA 328
DB 2969 TTGTATCCTTAACTCACTCAAGAACATCAACCAAAATTGCAAGGATTTGGGTAA 3028
QY 329 GAAACAATGCTCTCCTTGTAGCTTGTACATGAAGTGTAGTCAATGATGATGACACT 388
DB 3029 GAAACATCAACAACATCTCTCTGTGTGCAAGAAACGCGTAGTCATG-CCGAGATC 3087
QY 389 GATCCGATCTGATATATATATGCGCAATAGCTCACAAGCAACATTACAAACCCCATAC 448
DB 3088 ATACTCATCTGATATATCATG-CTTACAGCTCACAAG--ACATTACAAACAATC--AT 3140
QY 449 TATATACACAAAGTTTGTTCATGAAAAAACAATAAGTATGCAAGAGGGGACATATAT 508
DB 3141 ATTGCATTACCAAAATGTTTCAAGAAAAATAAAA---TAGGCGGACAGGACAAAAT 3196
QY 509 CCTTGCTTGAAGCGTAAAGTGAATTTTCAAGCCATATATACCTATATCTAATTATA 568
DB 3197 C-----CTTGACGTAAAGTAAATTATACAA---CAAAAAAACCATTATGTCAAGCTAA 3249
QY 569 AGTTGTTATATATATACGACGATGATCATCAACAACCGTACCTGTGAAAGGCAACAAAT 628
DB 3250 ATCTAATTGCTTTTACGTAAGTCAACAACCTGTA-----GAAAGGCAACAAAAT 3298
QY 629 GAGCCACGCAAAAAATGCAAGATGAATCATATGATGACGAAGCAATGCTGGCTTGTAC 688
DB 3299 GAGCCACGCAAGAAATGAGATGATTCAGATGA-----ACATGACACGTGTAC 3348
QY 689 ATAAAGTGAATGATGATCATTAATATTTGGCAAGAAACGTTGAAGCTACACAGCCGTG 748
DB 3349 GTAAAGAGATGAGATGATCATTAATTTGGCAAGAAACATGAAGCTGCTTACAGCCGT 3408
QY 749 GTCAATGACACAGGACACAAAGAACTGTG---CTAATCGAAGCTAATAATTAACCTTAG 804
DB 3409 CTCGTGGCATTAAGAAACAAAGAAATGTGTTAATATATCAAACTAATAATTAACGCTCG 3468
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QY 805 TATGCTATGACATTCCTCCATCACCACCATATATCTAGCTATTTACTCTCTTA 863
DB 3469 CATGCTGTGCACTTCTCCATCACCAACA-CTGGGCTTTCAGACCATTAAGCTTAATCTA 3526

RESULT 8
US-11-074-522-14
; Sequence 14, Application US/11074522
; Publication No. US20050198712A1
; GENERAL INFORMATION:
; APPLICANT: Syngenta Participations AG
; APPLICANT: Belts, Scott
; APPLICANT: Skalla, Dale
; APPLICANT: Voitrach, Sandra
; APPLICANT: Hendrickx, Koen
; TITLE OF INVENTION: O-PROTEIN SEQUENCE AND PROMOTER
; FILE REFERENCE: 1392/22/2
; CURRENT APPLICATION NUMBER: US/11/074,522
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US 60/551,286
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 11357
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificially constructed expression construct encoding a Nov9x
; OTHER INFORMATION: phytase with a gamma zein signal sequence under the control of
; OTHER INFORMATION: the gamma zein promoter
; NAME/KEY: misc feature
; LOCATION: (1)_(11357)
; OTHER INFORMATION: The sequence presented is of a circular molecule
US-11-074-522-14

Query Match      16.0%; Score 142.6; DB 24; Length 11357;
Best Local Similarity 65.3%; Pred. No. 2.2e-29;
Matches 430; Conservative 0; Mismatches 179; Indels 50; Gaps 13;

QY 214 CGTAAAGTGTAGGAAATACGAAACGAC---CATGGCATGTAGAGCTGTATGAATTGG 269
DB 91 CCTAAAGTGTAGGAAACAGAAACAACCATGATGGCATGTAAAGCTCCAAAGATTGG 150
QY 270 TGTATCCATACCAACAACCTGCCAGACATCAACAATTGCGACGTCAATGG-ATTGGGTCA 328
DB 151 TTGTATCCTTAACTCACTCAAGAACATCAACCAAAATTGCAAGGATTTGGGTAA 210
QY 329 GAAACAATGCTCTCCTTGTAGCTTGTACATGAAGTGTAGTCAATGATGATGACACT 388
DB 211 GAAACAATCAACAACATCTCTCTGTGTGCAAGAAACAGGTTAGTCATG-CCGAGATC 269
QY 389 GATCCGATCTGATATATATATGCGCAATAGCTCACAAGCAACATTAACAACCCCATAC 448
DB 270 ATACTCATCTGATATATCATG-CTTACAGCTCACAAG--ACATTACAAACAATC--AT 322
QY 449 TATATACACAAAGTTTGTTCATGAAAAAACAATAAGTATGCAAGAGGGGACATATAT 508
DB 323 ATTGCATTACCAAGATGCTTTCATGAAAAATAAAA---TAGGCGGACAGGACAAAAT 378
QY 509 CCTTGCTTGAAGCGTAAAGTGAATTTTCAAGCCATATATCAACCTATATCTAATTATA 568
DB 379 C-----CTTGACGTGTAAGTAAATTATACAA---CAAAAAAAGCCATATGTCAAGCTAA 431
QY 569 AGTTGTTATATATATACGACGATGATCATCAACAACCGTACCTGTGAAAGGCAACAAAT 628
DB 432 ATCTAATTGCTTTTACGTAAGTCAACAACCTGTA-----GAAAGGCAACAAAAT 480
QY 629 GAGCCACGCAAAAAATGCAAGATGAATCATATGATGACGAAGCAATGCTGGCTTGTAC 688
DB 481 GAGCCACGCAAGAGTACAGAAATGATTCAGATGA-----ACATGACAGTGTCTAC 530
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Qy 689 ATAAAGTAATGATGATCAATTAATTTGGCAAGAAACCGTGAAGCTACACAGCCGTC 748
    |||||
Db 531 GTAAAGAGATGACGATCATATATTTGGCAAGAAACCACTGAAGCTGCTACAGCGT 590
Qy 749 GTCAGTAGCAGAGAACACAGAAAGCTGTG---CTAATCGAAGCTTAATAAACCCTAG 804
    |||||
Db 591 CTCGGTGGCATTAAGAACACAGAAATTTGTTAATTAATCAAACTTAATAATAACGCTCG 650
Qy 805 TATGCCATGCACTTCTCCATCCAGCACTAACCCATATCTTCAGCTATTTACCTTCTCTA 863
    |||||
Db 651 CATGCCGTGCACTTCTCCATCCAGCACTAACCCATATCTTCAGCTATTTACCTTCTCTA 708
```

RESULT 9

```
US-11-074-522-17
; Sequence 17, Application US/11074522
; Publication No. US20050198712A1
; GENERAL INFORMATION:
; APPLICANT: Syngenta Participations AG
; APPLICANT: Betts, Scott
; APPLICANT: Skalla, Dale
; APPLICANT: Voltrach, Sandra
; APPLICANT: Hendrickx, Koen
; TITLE OF INVENTION: Q-PROTEIN SEQUENCE AND PROMOTER
; FILE REFERENCE: 1392/22/2
; CURRENT APPLICATION NUMBER: US/11/074,522
; PRIOR FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US 60/551,286
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 11888
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial Agrobacterium binary vector based on pMOV2117 into
; OTHER INFORMATION: which a Q-protein coding sequence has been inserted
; NAME/KEY: misc_feature
; LOCATION: (1)..(11888)
; OTHER INFORMATION: The sequence presented is of a circular molecule
US-11-074-522-17
```

```
Query Match 16.0%; Score 142.6; DB 24; Length 11888;
Best Local Similarity 65.3%; Pred. No. 2.2e-29;
Matches 430; Conservative 0; Mismatches 179; Indels 50; Gaps 13;

Qy 214 CGTAAAGTATGAGGAATACGGAACGAC---CATTGGCATGTAGAGCTGTATGAATTTGG 269
    |||||
Db 9411 CTTAAAGTGTGAGGAACAGAAACAAACATGATGGCATGTAAAGCTCCAGAAATTTG 9470
Qy 270 TGTATTCATACAACTCGCAGAACATCAAAAATTGCAAGCTCAATG-ATTGGGTCA 328
    |||||
Db 9471 TTGTATCTTAACTCAACAGAACATCAACCAAAATTGCAAGCTCAAGGTATTTGGTAA 9530
Qy 329 GAAACAATGCTCTCCCTTGTAGCTTGTACATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 388
    |||||
Db 9531 GAAACAATGCTCTCCCTTGTAGCTTGTACATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 9589
Qy 389 GATCCGATCTGATATATATGCAAAATAGCTCAGACGACGACGACGACGACGACGACGACGAC 448
    |||||
Db 9590 ATATCATCTGATATATATG-CTTACAGCTCACAAG---ACATTACAAACAATC---AT 9642
Qy 449 TATATCATCAAAAGTTGTTTCATGAAAAAAATTAATGATGACAGAGGGGACATATAT 508
    |||||
Db 9643 ATTGCATTACAAAGATCGTTTCATGAAAAATTAATA---TAGGCCGACAGACAAATAAT 9698
Qy 509 CCTTGCTTGACGCTTAAAGTGAATTTCAAAAGCATATATACCTATATATATATATA 568
    |||||
Db 9699 C---CTTGACGCTTAAAGTGAATTTTACAA---CAAAAAAAGCATATATATCAAGCTAA 9751
Qy 569 AGTTGTTATATATACGACGATGATCATCAAAACGTACCTGTGAAGGCAACAAAT 628
```

```
Db 9752 ATCTAATTCGTTTACGATATCAACAACTGTG-----GAAGCAACAAACT 9800
    |||||
Qy 629 GAGCCAGCAAAATAGCAATGATATTCATATATGACAGACGACCTGGCTTGTAC 688
    |||||
Db 9801 GAGCCAGCAAAATAGCAATGATATTCATATGACAGACGACCTGGCTTGTAC 9850
Qy 689 ATAAAGTAATGATGATCAATTAATTTGGCAAGAAACCGTGAAGCTACAGCCGTC 748
    |||||
Db 9851 GTAAAGAGATGACGATCATATATTTGGCAAGAAACCACTGAAGCTGCTACAGCGT 9910
    |||||
Qy 749 GTCAGTAGCAGAGAACACAGAAAGCTGTG---CTAATCGAAGCTTAATAAACCCTAG 804
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Db 9911 CTCGGTGGCATTAAGAACACAGAAATTTGTTAATTAATCAAACTTAATAATAACGCTCG 9970
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Qy 805 TATGCCATGCACTTCTCCATCCAGCACTAACCCATATCTTCAGCTATTTACCTTCTCTA 863
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RESULT 10

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US-10-311-455-1906/C
; Sequence 1906, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Deter-
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1906
; LENGTH: 19734
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1906
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Query Match 5.3%; Score 47.2; DB 15; Length 19734;
Best Local Similarity 46.6%; Pred. No. 0.061;
Matches 151; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

Qy 388 TGATCCATCTGATATATATGCCAAATAGCTCACACACACATTTACAAACCAACCCGATA 447
    |||||
Db 4680 TAAACCTTAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4621
Qy 448 CTATACATCAAAAGTTGTTTCATGAAAAAAACAAATAGATGACAGAGGACCAATTA 507
    |||||
Db 4620 CGACAAACAAACCCCATCTTAAACCAAAACCAAAACCAAAACCAAAACCAAAACCAAAAC 4561
Qy 508 TCCTTGCTTGAACGGTAAATGAAATTTACAAAGCATATATCAACTATATCTAATTAAT 567
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Db 4560 TCTACATTTATCTAATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 4501
Qy 568 AAGTTGCTTATATATACGACGATGATCATCAACACCGTACCTGTGAAGGCAACAAA 627
    |||||
Db 4500 TTCAATCTAATTAATTAAGAAATAATTAATTAATTAATTAATTAATTAATTAATTAAT 4441
Qy 628 TGAGCCAGCAAAATGACAGATGATCAATGATGATGATGATGATGATGATGATGATGATGAT 687
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Db 4440 AAAAAAATAATATACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4381
Qy 688 CATAAAGTGAATGATGATGATTAAT 711
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Db 4569 AAAAATAAAATAAAATTAACAAC 4543

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RESULT 14
US-10-311-455-1028/c
; Sequence 1028, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PREPERNBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detecting
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311.455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1028
; LENGTH: 6294
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1028
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Query Match 4.8%; Score 42.8; DB 15; Length 6294;
Best Local Similarity 48.0%; Pred. No. 0.62;
Matches 122; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 387 CTGATCCGATCTGATATATATGCGCAATAGCTCACAGCAACATTAACAACCCCAT 446
Db 2665 CTATATACCAATATAAATTAACCAAAAATTAACCAAAAATTAATCAATATCTACT 2606

QY 447 ACTATATACATCAAAAGTTTGTTCATGAAAAAACAATAAGTATGCGAGGAGCAATA 506
Db 2605 ACTCTAAAAAATAAATAAATAATTAACCAAAAATTAATAAATTCCTTAACAA 2546

QY 507 ATCCTTCTGACGCGTAAAGTGAATTACAAAGCCATATATCAACCTATATCTAATTAA 566
Db 2545 TCTCTAATATACCTTAAATTAATTTAAAAAATAAACAACAACTTATCTATAAT 2486

QY 567 TAAAGTTGTTATATATATACGACGATGATCAACAACCGTACCTGTGAAGGCAACAA 626
Db 2485 TTATATATAAATAAATAAACAACCAAAAATCAAAAACCAATTTCAACTTAACAAC 2426

QY 627 ATGAGCCACGCCAA 640
Db 2425 TCTATTCTCCTTA 2412
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RESULT 15
US-10-473-126-325/c
; Sequence 325, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/473.126
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 325
; LENGTH: 4165
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-325

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Best Local Similarity 47.1%; Pred. No. 0.66;
Matches 130; Conservative 0; Mismatches 146; Indels 0; Gaps 0;

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Db 2531 CACTACCCAAAAAATTCACAACATTAACCACTACAAAAAACCCTTCAAAAAACAA 2472

QY 445 ATACTATACATCAAAAGTTTGTTCATGAAAAAACAATAAGTATGCGAGGAGCA 504
Db 2471 ATCCTAACAACAACAAAAAATATCCCAATTAACCAAAATTAACCTCCCAATCAAAA 2412

QY 505 TAATCTTGTGACGCGTAAAGTGAATTACAAAGCCATATATCAACCTATATCTAAT 564
Db 2411 AATCACAATCCTTACTCAATATATTATTAATTCATACAAATACCAACCACTACTATTA 2352

QY 565 AATTAAGTTGTTATATATATACGACGATGATCAACAACCGTACCTGTGAAGGCAACA 624
Db 2351 ACAAAATTTGATTAATATACACAAATAATTAACAACCACTAATAAATAATCAACAAAAA 2292

QY 625 AAATGAGCCACGCCAAAAATTCAGAAATGATTCATAT 660
Db 2291 CTAACCAAAAAACAAAAACCCCTATTTCATCCCAAT 2256
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Search completed: September 24, 2005, 17:17.49
Job time : 681 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-10-660-097-8

Perfect score: 894
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Scoring table: OLIGO_NUC
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Searched: 4708233 seqs, 24227607955 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	894	100.0	894	6	BD226659 Methods a
2	894	100.0	894	6	AR411335 Sequence
3	411	46.0	412	6	BD226670 Methods a
4	411	46.0	412	6	AR411346 Sequence
5	221	24.7	222	6	BD226669 Methods a
6	221	24.7	222	6	AR411345 Sequence
7	30	3.4	489	8	AY294252 LOCUS
8	30	3.4	575	8	AJ629151 LOCUS
9	30	3.4	1051	8	AY566299 Methods b
10	30	3.4	2647	6	BD226673 Methods a
11	30	3.4	2647	6	AR411349 Sequence
12	30	3.4	2647	8	SVGKAF
13	24	2.7	290	8	AY294253
14	24	2.7	343	8	AY294251
15	24	2.7	3864	8	ZMZCI
16	23	2.6	31	6	BD226656 Methods a
17	23	2.6	31	6	BD226663 Methods a
18	23	2.6	31	6	AR411332 Sequence
19	23	2.6	31	6	AR411339 Sequence

C	20	2.5	11236	1	AE006188
C	21	2.5	91242	9	AP001252
C	22	2.5	148859	9	HSD7746R2
C	23	2.5	163328	2	AC016190
C	24	2.5	163689	9	BS000068
C	25	2.5	340000	9	AP001681
C	26	2.3	29	6	BD226657
C	27	2.3	29	6	BD226658
C	28	2.3	29	6	AR411333
C	29	2.3	29	6	AR411334
C	30	2.3	131566	2	AC151548
C	31	2.3	158375	2	CR456642
C	32	2.3	166617	2	CR450847
C	33	2.3	188285	9	AL135842
C	34	2.3	212597	2	AC105463
C	35	2.3	221116	5	AL845422
C	36	2.3	223295	2	BX649623
C	37	2.2	215	14	AB034415
C	38	2.2	215	14	AB034416
C	39	2.2	215	14	AB034417
C	40	2.2	215	14	AB034418
C	41	2.2	215	14	AB034419
C	42	2.2	215	14	AB034423
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ALIGNMENTS

RESULT 1	BD226659	894 bp	DNA	linear	PAT 17-JUN-2003
LOCUS	BD226659	894 bp	DNA	linear	PAT 17-JUN-2003
DEFINITION	Methods and compositions for expression of transgenes in plants.				
ACCESSION	BD226659.1	GI:33036429			
VERSION	JP 2002533057-A/8.				
KEYWORDS	JP 2002533057-A/8.				
SOURCE	synthetic construct				
ORGANISM	other sequences; artificial sequences.				
REFERENCE	1 (bases 1 to 894)				
AUTHORS	Kriz,A.L., Luethy,M.H. and Voyles,D.A.				
TITLE	Methods and compositions for expression of transgenes in plants				
JOURNAL	Patent: JP 2002533057-A 8 08-OCT-2002;				
COMMENT	DEKALB GENETICS CORP				
OS	Artificial Sequence				
PN	JP 2002533057-A/8				
PD	08-OCT-2002				
PF	14-MAY-1999				
PR	14-MAY-1998				
PI	ALAN L KRIZ, MICHAEL H LUETHY, DALE A VOYLES				
PC	AO1H1/00, C12N5/10, C12N5/09, C12N5/00, C12N15/00 CC				
Description of Artificial Sequence: Synthetic Primer FH					
Location/Qualifiers					
FT	source	1..894			
Location/Qualifiers					
1..894					
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/mol_type="genomic DNA"					
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ORIGIN					
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Best Local Similarity	100.0%;	Score 894;	DB 6;	Length 894;	
Matches 894;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	GGACCGGTTACACACCACTGTGGTGTCTTCAAGGACGATCAAACTATGATCATCA	60		
Db	1	GGACCGGTTACACACCACTGTGGTGTCTTCAAGGACGATCAAACTATGATCATCA	60		
OY	61	TATAGCAGCAATCACTCTTGTCTTACAGACAGACCAATGATCATCACTTCAAGG	120		

Db 61 TATAGCAGCAGAACTCACTCTCTTCTCTACAGACAAACCAATGCATCACTTCAAGG 120
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Db 121 AGTACGAGCGCTCTTCTTGTACTGTCTTTCAGAAATTGGSCATTTCTTGTGGAAGCATGCA 180
Qy 181 GTGTAGGTTCTCACTTCAAGGATTAATCTGACACGTAAAGTGAAGGAAATACGGAACGA 240
Db 181 GTGTAGGTTCTCACTTCAAGGATTAATCTGACACGTAAAGTGAAGGAAATACGGAACGA 240
Qy 241 CCATTGGCATGTAGAGCTGTATGAAATGGTTATTCATACAACTCCGAGAACATCA 300
Db 241 CCATTGGCATGTAGAGCTGTATGAAATGGTTATTCATACAACTCCGAGAACATCA 300
Qy 301 CAAAATTGCAAGTCAATGGAATGGGTGAGAAACAAATGCTCTCTTGTAGCTGTACAT 360
Db 301 CAAAATTGCAAGTCAATGGAATGGGTGAGAAACAAATGCTCTCTTGTAGCTGTACAT 360
Qy 361 GAAGTGTGTGATGATCACTGATCCGATCCGATGATATATATATGCAAAATAGTCA 420
Db 361 GAAGTGTGTGATGATCACTGATCCGATCCGATGATATATATATGCAAAATAGTCA 420
Qy 421 CACGACAACTTACAAACAAACCCCATCTATACATCAAAAGTTTGTGATGAAAC 480
Db 421 CACGACAACTTACAAACAAACCCCATCTATACATCAAAAGTTTGTGATGAAAC 480
Qy 481 AATAAGTATGACAGAGAGGACAAATTAATCTCTGCTTGAACGATGAATTTACAAG 540
Db 481 AATAAGTATGACAGAGAGGACAAATTAATCTCTGCTTGAACGATGAATTTACAAG 540
Qy 541 CCATATATCAACCTATATCTAATTAATGATGCTTATATATATGACGAGATGATCA 600
Db 541 CCATATATCAACCTATATCTAATTAATGATGCTTATATATATGACGAGATGATCA 600
Qy 601 CAACCGTACCTGTGAAAGGCAAAATGAGCCACGCAAAATGCAAGATGATCAAT 660
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Qy 661 GATGACGAGATGACCTGCGCTTGTCTATTAATGATGAATGATGATCAATTTTGGC 720
Db 661 GATGACGAGATGACCTGCGCTTGTCTATTAATGATGAATGATGATCAATTTTGGC 720
Qy 721 AAGAAACCGTGAAGCTACACAGCGCTGTGATGACACAGAAACAGAAATCTGCT 780
Db 721 AAGAAACCGTGAAGCTACACAGCGCTGTGATGACACAGAAACAGAAATCTGCT 780
Qy 781 AATGAGCTATTAATTAACCTAGTATGCTATGCACTTCTCATCACTACCATCATAT 840
Db 781 AATGAGCTATTAATTAACCTAGTATGCTATGCACTTCTCATCACTACCATCATAT 840
Qy 841 CTTGAGCTATTTAATCTTCTATCTACTCCAGAGAGACAGAAAGATGACACC 894
Db 841 CTTGAGCTATTTAATCTTCTATCTACTCCAGAGAGACAGAAAGATGACACC 894

RESULT 2
LOCUS AR411335 894 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 8 from patent US 6635806.
ACCESSION AR411335
VERSION AR411335.1 GI:40163439
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1. (bases 1 to 894)
AUTHORS Kriz, A.L., Ineithy, M.H. and Voyles, D.A.
TITLE Methods and compositions for expression of transgenes in plants
JOURNAL Patent: US 6635806-A 8 21-OCT-2003;
FEATURES
source 1. .894
/organism="unknown"

ORIGIN /mol_type="genomic DNA"
Query Match 100.0%; Score 894; DB 6; Length 894;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 894; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGAACGGTTACAGACACCACTGGGTGGTCTCAAGGACAGTACCAATATGATCA 60
Db 1 GGAACGGTTACAGACACCACTGGGTGGTCTCAAGGACAGTACCAATATGATCA 60
Qy 61 TATAGCAGCAGAACTCACTGTCTTGTCTACAGACAAACCAATGATCACTTCAAGG 120
Db 61 TATAGCAGCAGAACTCACTGTCTTGTCTACAGACAAACCAATGATCACTTCAAGG 120
Qy 121 AGTACGAGCGCTCTTCTTGTACTGTCTTTCAGAAATTGGSCATTTCTTGTGGAAGCATGCA 180
Db 121 AGTACGAGCGCTCTTCTTGTACTGTCTTTCAGAAATTGGSCATTTCTTGTGGAAGCATGCA 180
Qy 181 GTGTAGGTTCTCACTTCAAGGATTAATCTGACACGTAAAGTGAAGGAAATACGGAACGA 240
Db 181 GTGTAGGTTCTCACTTCAAGGATTAATCTGACACGTAAAGTGAAGGAAATACGGAACGA 240
Qy 241 CCATTGGCATGTAGAGCTGTATGAAATGGTTATTCATACAACTCCGAGAACATCA 300
Db 241 CCATTGGCATGTAGAGCTGTATGAAATGGTTATTCATACAACTCCGAGAACATCA 300
Qy 301 CAAAATTGCAAGTCAATGGAATGGGTGAGAAACAAATGCTCTCTTGTAGCTGTACAT 360
Db 301 CAAAATTGCAAGTCAATGGAATGGGTGAGAAACAAATGCTCTCTTGTAGCTGTACAT 360
Qy 361 GAAGTGTGTGATGATCACTGATCCGATCCGATGATATATATGCAAAATAGTCA 420
Db 361 GAAGTGTGTGATGATCACTGATCCGATCCGATGATATATATGCAAAATAGTCA 420
Qy 421 CACGACAACTTACAAACAAACCCCATCTATACATCAAAAGTTTGTGATGAAAC 480
Db 421 CACGACAACTTACAAACAAACCCCATCTATACATCAAAAGTTTGTGATGAAAC 480
Qy 481 AATAAGTATGACAGAGAGGACAAATTAATCTCTGCTTGAACGATGAATTTACAAG 540
Db 481 AATAAGTATGACAGAGAGGACAAATTAATCTCTGCTTGAACGATGAATTTACAAG 540
Qy 541 CCATATATCAACCTATATCTAATTAATGATGCTTATATATGACGAGATGATCA 600
Db 541 CCATATATCAACCTATATCTAATTAATGATGCTTATATATGACGAGATGATCA 600
Qy 601 CAACCGTACCTGTGAAAGGCAAAATGAGCCACGCAAAATGCAAGATGATCAAT 660
Db 601 CAACCGTACCTGTGAAAGGCAAAATGAGCCACGCAAAATGCAAGATGATCAAT 660
Qy 661 GATGACGAGATGACCTGCGCTTGTCTATTAATGATGAATGATGATCAATTTTGGC 720
Db 661 GATGACGAGATGACCTGCGCTTGTCTATTAATGATGAATGATGATCAATTTTGGC 720
Qy 721 AAGAAACCGTGAAGCTACACAGCGCTGTGATGACACAGAAACAGAAATCTGCT 780
Db 721 AAGAAACCGTGAAGCTACACAGCGCTGTGATGACACAGAAACAGAAATCTGCT 780
Qy 781 AATGAGCTATTAATTAACCTAGTATGCTATGCACTTCTCATCACTACCATCATAT 840
Db 781 AATGAGCTATTAATTAACCTAGTATGCTATGCACTTCTCATCACTACCATCATAT 840
Qy 841 CTTGAGCTATTTAATCTTCTATCTACTCCAGAGAGACAGAAAGATGACACC 894
Db 841 CTTGAGCTATTTAATCTTCTATCTACTCCAGAGAGACAGAAAGATGACACC 894

RESULT 3
LOCUS BD226670 412 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods and compositions for expression of transgenes in plants.
ACCESSION BD226670

VERSION	KEYWORDS
BD226670.1	GI:33036440
SOURCE	ORGANISM
JP 2002533057-A/19.	synthetic construct
	synthetic construct
	other sequences; artificial sequences.
REFERENCE	AUTHORS
1 (bases 1 to 412)	Kritz,A.L., Luethy,M.H. and Voyles,D.A.
TITLE	JOURNAL
Methods and compositions for expression of transgenes in plants	Patent: JP 2002533057-A 19 08-Oct-2002;
COMMENT	DERALB GENETICS CORP OS Artificial Sequence PN JP 2002533057-A/19 PD 08-OCT-2002 PF 14-MAY-1999 JP 2000548450 PR 14-MAY-1998 US 09/078972 PI ALAN L KRIZ,MICHAEL H LUETHY,DALE A VOYLES PC A01H1/0,C12N5/10,C12M15/09,C12M5/00,C12N15/00 CC Description of Artificial Sequence: Synthetic Primer FH Key
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FT	Location/Qualifiers
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	1..412
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	/mol_type='genomic DNA'
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Query Match	46.0%; Score 411; DB 6; Length 412;
Best Local Similarity	100.0%; Pred. No. 1,6e-220; Indels 0; Gaps 0;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	484 TAACTATGACAGAGGGAGCAATAATCCTTGTGTCGCGTAAGTGAATTACAAGCCA 543
Dd	2 TAACTATGACAGAGGGAGCAATAATCCTTGTGTCGCGTAAGTGAATTACAAGCCA 61
OY	544 TATATCAACTATATCTTAATTAATGTTGGTTATATATACGCAGATCATCAACA 603
Dd	62 TATATCAACTATATCTTAATTAATGTTGGTTATATATACGCAGATCATCAACA 121
OY	604 CCGTACCCTGTGAAGGCCAACAAAATGAGCCACGCAAAAAATGCAGATGATCATATGAT 663
Dd	122 CCGTACCCTGTGAAGGCCAACAAAATGAGCCACGCAAAAAATGCAGATGATCATATGAT 181
OY	664 GACCAAGCTACACTCGGCTTGCTCATTAATGATGATGATGATGATTAATTTTGGCAAG 723
Dd	182 GACCAAGCTACACTCGGCTTGCTCATTAATGATGATGATGATGATTAATTTTGGCAAG 241
OY	724 AAACCGTGAAGAAGCTACACAGCCGCTGCTGATGACACAGAAACACAGAATCTGTCTAAT 783
Dd	242 AAACCGTGAAGAAGCTACACAGCCGCTGCTGATGACACAGAAACACAGAATCTGTCTAAT 301
OY	784 CGAAGCTATAATAATTAACCTAGTAGCCATGACCTTCATCACTACCACTATCCATATCTT 843
Dd	302 CGAAGCTATAATAATTAACCTAGTAGCCATGACCTTCATCACTACCACTATCCATATCTT 361
OY	844 CAGCTATATTTACCTTCTCTATCTACTCTCAGAGAGACACAGAATGACACAC 894
Dd	362 CAGCTATATTTACCTTCTCTATCTACTCTCAGAGAGACACAGAATGACACAC 412
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LOCUS AR411346	412 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 19 from patent US 6655806.	
ACCESSION AR411346	
VERSION AR411346.1	GI:40163450
KEYWORDS	
SOURCE Unknown.	
ORGANISM Unknown.	
REFERENCE 1 (bases 1 to 412)	
Kritz,A.L., Luethy,M.H. and Voyles,D.A.	

TITLE	Methods and compositions for expression of transgenes in plants
JOURNAL	Patent: US 6635806-A 19 21-OCT-2003;
FEATURES	Location/Qualifiers 1..412 /organism="unknown" /mol_type="genomic DNA"
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Query Match	46.0%; Score 411; DB 6; Length 412;
Best Local Similarity	100.0%; Pred. No. 1.ee-220;
Matches	411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	484 TAACTATGACGAGGAGGACAAATAATCTCTTGCTTGACGGCTAAAGTGAATTTACAAAGCCA 543
DB	2 TAACTATGACGAGGAGGAGCAATAATCTCTTGCTTGACGGCTAAAGTGAATTTACAAAGCCA 61
OY	544 TATATCAACCTATATATTAATTAATAGTTCGTTATATATATATACGACGATGATCATCAACAA 603
DB	62 TATATCAACCTATATATTAATTAATAGTTCGTTATATATATACGACGATGATCATCAACAA 121
OY	604 CCGTACCTGTGAAAGGCAACAAATGAGCCACGCAAAAATCAGAAATGATTCATATGAT 663
DB	122 CCGTACCTGTGAAAGGCAACAAATGAGCCACGCAAAAATCAGAAATGATTCATATGAT 181
OY	664 GACGACGCTACACTCGGCTTGCTATCATTAAGTAATGATGATCATTAATATTTGGCAAG 723
DB	182 GACCAACGCTACACTCGGCTTGCTATCATTAAGTAATGATGATCATTAATATTTGGCAAG 241
OY	724 AAACCGTGAAGCTACACAGCGCGTCGATGAGCAACGGAACACAGAAGATGTGCTAAT 783
DB	242 AAACCGTGAAGCTACACAGCGCGTCGATGAGCAACGGAACACAGAAGATGTGCTAAT 301
OY	784 CGAAGCTATTAATAACCTAGTATGCTATGCTCATCTTCATCAACCACTACCATATCTT 843
DB	302 CGAAGCTATTAATAACCTAGTATGCTATGCTCATCTTCCTCATACCACTACCATATCTT 361
OY	844 CAGTCTATTTACCTTCTCTATCTACTCCAGAGCACAGAAAGATGCACCC 894
DB	362 CAGTCTATTTACCTTCTCTATCTACTCCAGAGCACAGAAAGATGCACACC 412
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DEFINITION	Methods and compositions for expression of transgenes in plants.
ACCESSION	BD226669
VERSION	BD226669.1 GI:33036439
KEYWORDS	JP 2002533057-A/18.
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	1 (bases 1 to 222)
AUTHORS	Kriz,A.L., Luethy,M.H. and Voyles,D.A.
TITLE	Methods and compositions for expression of transgenes in plants
JOURNAL	Patent: JP 2002533057-A 18 08-OCT-2002;
COMMENT	DEKALB GENETICS CORP OS Artificial Sequence PN JP 2002533057-A/18
PD	08-OCT-2002
PF	14-MAY-1999 JP 2000548450
PR	14-MAY-1998 US 09/078972
PI	ALAN L KRIZ,MICHAEL H LUEETHY,DALE A VOYLES
PC	AO1H1/0,C12N5/10,C12N15/09,C12N15/00,C12N15/00 CC
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FEATURES	Location/Qualifiers 1..222 /organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630"
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Best Local Similarity 100.0%; Pred. No. 6.3e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      522 GTAAAGTGAATTTACAAAGCCATATATCAA 551
DB      156 GTAAAGTGAATTTACAAAGCCATATATCAA 185

RESULT 9
LOCUS      AY566299
DEFINITION Sorghum bicolor clone MML-07 gamma kafirin protein gene, partial
c88.
ACCESSION      AY566299
VERSION      GI:45645343
KEYWORDS
SOURCE
ORGANISM      Sorghum bicolor (sorghum)
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              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
              clade; Panicoideae; Andropogoneae; Sorghum.
              1 (bases 1 to 1051)
              Banaei,S., Mishra,A., Khanna,V.K. and Garg,G.K.
              Partial sequence of gamma kafirin gene
              Unpublished
              2 (bases 1 to 1051)
              Banaei,S., Mishra,A., Khanna,V.K. and Garg,G.K.
              Direct Submission
              Submitted (03-MAR-2004) Dept. of Molecular Biology and Genetic
              Engineering, GBUVAT, Pantnagar, US Nagar, Uttaranchal 263145, India
              Location/Qualifiers
                1..1051
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Query Match      3.4%; Score 30; DB 8; Length 1051;
Best Local Similarity 100.0%; Pred. No. 6.3e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      156 GTAAAGTGAATTTACAAAGCCATATATCAA 185

RESULT 10
LOCUS      BD226673
DEFINITION Methods and compositions for expression of transgenes in plants.
ACCESSION      BD226673
VERSION      BD226673.1 GI:33036443
KEYWORDS      JP 2002533057-A/22.
              JP 2002533057-A/22.
              synthetic construct
              other sequences; artificial sequences.
              1 (bases 1 to 2647)
              Kriz,A.L., Luethy,M.H. and Voyles,D.A.
              Methods and compositions for expression of transgenes in plants
              Patent: JP 2002533057-A 22 08-OCT-2002;
              DEKALB GENETICS CORP
              OS Artificial Sequence
              PN JP 2002533057-A/22
              PD 08-OCT-2002
              PF 14-MAY-1999 JP 2000548450
              PR 14-MAY-1998 US 09/078972
              PI ALAN L KRIZ,MICHAEL H LUETHY,DALE A VOYLES
              PC A01H1/00,C12N5/09,C12N15/00,C12N15/00 CC
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Best Local Similarity 100.0%; Pred. No. 6.2e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      522 GTAAAGTGAATTTACAAAGCCATATATCAA 551
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RESULT 11
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DEFINITION Sequence 22 from patent US 6635806.
ACCESSION      AR411349
VERSION      AR411349.1 GI:40163453
KEYWORDS
SOURCE
ORGANISM      Unknown.
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              Unclassified.
              1 (bases 1 to 2647)

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AUTHORS Kriz,A.L., Luechy,M.H. and Voyles,D.A.
 TITLE Methods and compositions for expression of transgenes in plants
 JOURNAL Patent: US 6635806-A 22 21-OCT-2003;
 FEATURES Location/Qualifiers
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 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 3.4%; Score 30; DB 6; Length 2647;
 Best Local Similarity 100.0%; Pred. No. 6.2e-05;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 522 GTAAGTGAATTTCACAAAGCCATATATCAA 551
 Db 886 GTAAGTGAATTTCACAAAGCCATATATCAA 915

RESULT 12

LOCUS SUGKAP 2647 bp DNA linear PLN 13-FEB-1995
 DEFINITION S.vulgare gene for gamma-kafirin.
 ACCESSION X62480
 VERSION X62480.1 GI:671655
 KEYWORDS gamma-kafirin; gamma-prolamins; seed storage protein.
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 2647)
 de Freitas,F.A., Vunes,J.A., da Silva,M.J., Arruda,P. and Leite,A.
 Structural characterization and promoter activity analysis of the
 gamma-kafirin gene from sorghum
 Mol. Gen. Genet. 245 (2), 177-186 (1994)

REFERENCE
 AUTHORS 1 (bases 1 to 2647)
 TITLE Direct Submission
 JOURNAL Submitted (07-OCT-1991) A. Leite, Centro de Biologia Molecular &
 Engenharia Genetica, Universidade Estadual de Campinas, Cidade
 Universitaria 'Zeferino Vas', Cep 13.081-Campinas-Sao Paulo, BRAZIL
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 1224..1859
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 mat_peptide
 polyA_signal
 polyA_signal

ORIGIN

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 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 522 GTAAGTGAATTTCACAAAGCCATATATCAA 551
 Db 886 GTAAGTGAATTTCACAAAGCCATATATCAA 915

RESULT 13

LOCUS AY294253 290 bp DNA linear PLN 05-AUG-2003
 DEFINITION Sorghum bicolor gamma kafirin gene, promoter MML 01 region.
 ACCESSION AY294253
 VERSION AY294253.1 GI:31580637
 KEYWORDS
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 290)
 Mishra,A., Singh,B.K., Bhadana,V., Shallesh,G., Khanna,V.K. and
 Garg,G.K.
 Gamma kafirin gene promoter (Kaf Prom MML 01) of Sorghum bicolor
 M35-1
 Unpublished
 2 (bases 1 to 290)
 Mishra,A., Singh,B.K., Bhadana,V., Shallesh,G., Khanna,V.K. and
 Garg,G.K.
 Direct Submission
 TITLE Submitted (09-MAY-2003) Molecular Biology and Genetic Engineering,
 G. B. Pant University of Agriculture and Technology, Pantnagar, U S
 Negar, Uttaranchal 261145, India
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 Db 174 GCCTATGCACCTTCATCACCAC 197

RESULT 14

LOCUS AY294251 343 bp DNA linear PLN 30-JUN-2003
 DEFINITION Sorghum bicolor gamma kafirin gene, promoter MML 02 region.
 ACCESSION AY294251
 VERSION AY294251.1 GI:31580635
 KEYWORDS
 SOURCE Sorghum bicolor (sorghum)
 ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 343)
 Mishra,A., Singh,B.K., Bansal,S., Khanna,V.K. and Garg,G.K.
 Gamma kafirin gene promoter (Kaf Prom MML 02) of Sorghum bicolor

REFERENCE
 AUTHORS 1 (bases 1 to 343)
 TITLE Direct Submission

JOURNAL M35-1
 REFERENCE 2 (bases 1 to 343)
 AUTHORS Mishra,A., Singh,B.K., Bansal,S., Khanna,V.K. and Garg,G.K.
 TITLE Direct Submission
 JOURNAL Submitted (09-MAY-2003) Molecular Biology and Genetic Engineering,
 G. B. Pant University of Agriculture and Technology, Pantnagar, U S
 Nagar, Uttaranchal 263145, India

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RESULT 15
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 DEFINITION Maize Zc1 gene for Zein Zc1 (14 kD zein-2).
 ACCESSION X53515
 VERSION X53515.1 GI:22514
 KEYWORDS storage protein; Zc1 gene; zein protein.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 3864)
 Reina,M., Guillen,P., Ponte,I., Boronat,A. and Palau,J.
 DNA sequence of the gene encoding the Zc1 protein from Zea mays W64
 A

REFERENCE
 AUTHORS Reina,M., Guillen,P., Ponte,I., Boronat,A. and Palau,J.
 TITLE Nucleic Acids Res. 18 (21), 6425 (1990)
 JOURNAL MEDLINE 91057131
 MEDLINE 2243787
 PUBMED 2 (bases 1 to 3864)
 REFERENCE 2 (bases 1 to 3864)
 AUTHORS Reina,M.
 TITLE Direct Submission
 JOURNAL Submitted (23-JUN-1990) Reina M., Dept. of Biología Molecular,
 C.I.D., C.S.I.C. Jordi Girona Salgado 18-26, 08034 Barcelona, Spain

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QY 283 ACAACTCGCAGAACATCACAAT 306
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 Db 757 ACAACTCGCAGAACATCACAAT 780

Search completed: September 24, 2005, 18:32:19
 Job time : 3915 secs

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CC Coix promoter, and then regenerating a monocotyledonous plant which
 CC expresses the gene from the recipient cell. The method can be used to
 CC prevent gene silencing in a monocotyledonous plant. The methods can be
 CC used for transforming monocot plants such as rice, wheat, oats, barley,
 CC rye, sorghum and maize. They can be transformed with genes such as an
 CC insect resistance gene, a fungal disease resistance gene, a viral disease
 CC resistance gene, a bacterial disease resistance gene, a herbicide
 CC resistance gene, a gene affecting grain composition or quality, a
 CC nutrient utilization gene, a mycotoxin reduction gene, a male sterility
 CC gene, a selectable marker gene, a screenable marker gene, a negative
 CC selectable marker gene, a gene affecting plant agronomic characteristics,
 CC and an environment or stress resistance gene. The methods can also be
 CC used for producing transgenic dicot plants such as tobacco, tomato,
 CC potato, soybean and cotton
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 DB 61 TATAGCAGCAATCACCTGCTTGTCTACAGACAGAACCAATGCATCACTCAAGG 120
 QY 121 AGTACGACGCTCTTCTGACTGTCTTCAGAAATGTGGCATTTCTGTGGAAGCATAGCA 180
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 DB 601 CAACCGTACCTGTAAAGGCAAAATAGACCCAGCAAAATGAGAAATGCAATTCATAT 660
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 AC AA245484;
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 DT 06-APR-2000 (first entry)
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 DE Fragment of the gamma-coixin gene promoter.
 XX
 KW Gamma-coixin protein; monocotyledonous plant; Coix promoter;
 KW gene silencing; rice; wheat; oat; barley; rye; sorghum; maize;
 KW insect resistance; fungal disease resistance; viral disease resistance;
 KW bacterial disease resistance; herbicide resistance; grain composition;
 KW nutrient utilization; mycotoxin reduction; male sterility;
 KW stress resistance; transgenic plant; ss.
 XX
 OS Coix lacryma-jobi.
 XX
 PN MO9958659-A2.
 PD 18-NOV-1999.
 XX
 PE 14-MAY-1999; 99NO-US010776.
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 PR 14-MAY-1998; 98US-00078972.
 XX
 PA (DEKA-) DEKALB GENETICS CORP.
 XX
 PI Kriz AL, Luethy MH, Voyles DA;
 DR WPI; 2000-126367/11.
 XX
 PT New isolated Coix regulatory sequences, used for producing transgenic
 PT plants with improved properties.
 XX
 PS Claim 37; Page 233; 238pp; English.
 XX
 CC The present sequence represents a fragment of the gamma-coixin promoter.
 CC The promoter is used in the method of the invention. The specification
 CC describes a method of preparing a monocotyledonous plant (other than Coix
 CC sp.) expressing a selected gene. The method comprises transforming a
 CC plant cell with construct comprising a selected gene operably linked to a
 CC Coix promoter, and then regenerating a monocotyledonous plant which
 CC expresses the gene from the recipient cell. The method can be used to
 CC prevent gene silencing in a monocotyledonous plant. The methods can be
 CC used for transforming monocot plants such as rice, wheat, oats, barley,
 CC rye, sorghum and maize. They can be transformed with genes such as an
 CC insect resistance gene, a fungal disease resistance gene, a viral disease
 CC resistance gene, a bacterial disease resistance gene, a herbicide
 CC resistant utilization gene, a mycotoxin reduction gene, a male sterility
 CC gene, a selectable marker gene, a screenable marker gene, a negative
 CC selectable marker gene, a gene affecting plant agronomic characteristics,
 CC and an environment or stress resistance gene. The methods can also be
 CC used for producing transgenic dicot plants such as tobacco, tomato,
 CC potato, soybean and cotton
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RESULT 3
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ID AAZ45483 standard; DNA; 222 BP.
AC AAZ45483;
XX
DT 06-APR-2000 (first entry)
XX
DE Fragment of the gamma-coixin gene promoter.
XX
KW Gamma-coixin protein; monocotyledonous plant; Coix promoter;
KW gene silencing; rice; wheat; oat; barley; rye; sorghum; maize;
KW insect resistance; fungal disease resistance; viral disease resistance;
KW bacterial disease resistance; herbicide resistance; grain composition;
KW nutrient utilization; mycotoxin reduction; male sterility;
KW stress resistance; transgenic plant; ss.
XX
OS Coix lacryma-jobi.
XX
PN WO9958659-A2.
XX
PD 18-NOV-1999.
XX
PF 14-MAY-1999; 99MO-US010776.
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PR 14-MAY-1998; 98US-00078972.
XX
PA (DEKA-) DEKALB GENETICS CORP.
XX
PI Kriz AL, Luethy MH, Voyles DA;
XX
DR WPI; 2000-126367/11.
XX
PT New isolated Coix regulatory sequences, used for producing transgenic
PS plants with improved properties.
XX
PS Claim 35; Page 232-233; 238pp; English.
XX
CC The present sequence represents a fragment of the gamma-coixin promoter.
CC The promoter is used in the method of the invention. The specification
CC describes a method of preparing a monocotyledonous plant (other than Coix
CC sp.) expressing a selected gene. The method comprises transforming a
CC plant cell with construct comprising a selected gene operably linked to a
CC Coix promoter, and then regenerating a monocotyledonous plant which
```

```
CC expresses the gene from the recipient cell. The method can be used to
CC prevent gene silencing in a monocotyledonous plant. The methods can be
CC used for transforming monocot plants such as rice, wheat, oats, barley,
CC rye, sorghum and maize. They can be transformed with genes such as an
CC insect resistance gene, a fungal disease resistance gene, a viral disease
CC resistance gene, a bacterial disease resistance gene, a herbicide
CC resistance gene, a gene affecting grain composition or quality, a
CC nutrient utilization gene, a mycotoxin reduction gene, a male sterility
CC gene, a selectable marker gene, a screenable marker gene, a negative
CC selectable marker gene, a gene affecting plant agronomic characteristics,
CC and an environment or stress resistance gene. The methods can also be
CC used for producing transgenic dicot plants such as tobacco, tomato,
CC potato, soybean and cotton
XX
SQ Sequence 222 BP; 73 A; 59 C; 37 G; 53 T; 0 U; 0 Other;
XX
Query Match 24.7%; Score 221; DB 3; Length 222;
Best Local Similarity 100.0%; Pred.No.3.1e-104;
Matches 221; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 674 CACTCGGCTTGCTACATTAAGTGAATGATGATCATTAATTTGGCAAGAACCGTGAA 733
    |||
    |||
    |||
Db 2 CACTCGGCTTGCTACATTAAGTGAATGATGATCATTAATTTGGCAAGAACCGTGAA 61
    |||
    |||
    |||
QY 734 AGCTACACAGCCCGCTGCTACAGACAGAAACAAATGCTAATGGAAGCTATA 793
    |||
    |||
    |||
Db 62 AGCTACACAGCCCGCTGCTACAGACAGAAACAAATGCTAATGGAAGCTATA 121
    |||
    |||
    |||
QY 794 AATAACCTAGTATGCTATGCACTTCCATCACTACCTCATATCTTCACTATTT 853
    |||
    |||
    |||
Db 122 AATAACCTAGTATGCTATGCACTTCCATCACTACCTCATATCTTCACTATTT 181
    |||
    |||
    |||
QY 854 ACCTTCTCTATCTACTCCAGAGACAGAAAGATCGACACC 894
    |||
    |||
    |||
Db 182 ACCTTCTCTATCTACTCCAGAGACAGAAAGATCGACACC 222
    |||
    |||
    |||

RESULT 4
AAZ45477
ID AAZ45477 standard; DNA; 31 BP.
AC AAZ45477;
XX
DT 06-APR-2000 (first entry)
XX
DE PCR primer gcx-1000seq5'xho for the gamma-coixin protein coding DNA.
XX
KW Gamma-coixin protein; monocotyledonous plant; Coix promoter;
KW gene silencing; rice; wheat; oat; barley; rye; sorghum; maize;
KW insect resistance; fungal disease resistance; viral disease resistance;
KW bacterial disease resistance; herbicide resistance; grain composition;
KW nutrient utilization; mycotoxin reduction; male sterility;
KW stress resistance; transgenic plant; PCR primer; ss.
XX
OS Coix lacryma-jobi.
XX
PN WO9958659-A2.
XX
PD 18-NOV-1999.
XX
PF 14-MAY-1999; 99MO-US010776.
XX
PR 14-MAY-1998; 98US-00078972.
XX
PA (DEKA-) DEKALB GENETICS CORP.
XX
PI Kriz AL, Luethy MH, Voyles DA;
XX
DR WPI; 2000-126367/11.
XX
PT New isolated Coix regulatory sequences, used for producing transgenic
PS plants with improved properties.
XX
```

PS Example 2; Page 156; 238pp; English.

XX PCR primers AA25477-78 were used to amplify the coding region of the gamma-coixin gene for subsequent cloning. The amplified fragment is used in the course of the invention. The specification describes a method of preparing a monocotyledonous plant (other than Coix sp.) expressing a selected gene. The method comprises transforming a plant cell with a construct comprising a selected gene operably linked to a Coix promoter, and then regenerating a monocotyledonous plant which expresses the gene from the recipient cell. The method can be used to prevent gene silencing in a monocotyledonous plant. The methods can be used for transforming monocot plants such as rice, wheat, oats, barley, rye, sorghum and maize. They can be transformed with genes such as an insect resistance gene, a fungal disease resistance gene, a viral disease resistance gene, a bacterial disease resistance gene, a herbicide resistance gene, a gene affecting grain composition or quality, a nutrient utilization gene, a mycotoxin reduction gene, a male sterility gene, a selectable marker gene, a screenable marker gene, a negative selectable marker gene, a gene affecting plant agronomic characteristics, and an environment or stress resistance gene. The methods can also be used for producing transgenic dicot plants such as tobacco, tomato, potato, soybean and cotton.

SQ Sequence 31 BP; 7 A; 10 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 2.6%; Score 23; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGACCGGTTACGACACCACTG 23
AA245470
ID AA245470 standard; DNA; 31 BP.
XX
AC AA245470;
XX
DT 06-APR-2000 (first entry)
XX
DE PCR primer gcx-1000seq5'xho for the gamma-coixin gene promoter.

XX Gamma-coixin protein; monocotyledonous plant; Coix promoter;
KW gene silencing; rice; wheat; oat; barley; rye; sorghum; maize;
KW insect resistance; fungal disease resistance; viral disease resistance;
KW bacterial disease resistance; herbicide resistance; grain composition;
KW nutrient utilization; mycotoxin reduction; male sterility;
KW stress resistance; transgenic plant; PCR primer; ss.
XX
OS Coix lacryma-jobi.
XX
PN WO958659-A2.
XX
PD 18-NOV-1999.
XX
PP 14-MAY-1999; 99WO-US010776.
XX
PR 14-MAY-1998; 98US-00078972.
XX
PA (DEKA-) DEKALB GENETICS CORP.
XX
PI Kriz AL, Luethy MH, Voyles DA;
XX
DR WPI; 2000-126367/11.
XX
PT New isolated Coix regulatory sequences, used for producing transgenic plants with improved properties.
XX
PS Example 1; Page 153; 238pp; English.
XX
CC PCR primers AA245470-72 were used to amplify the promoter of the gamma-coixin gene for subsequent cloning. The promoter is used in the method of

CC the invention. The specification describes a method of preparing a monocotyledonous plant (other than Coix sp.) expressing a selected gene. The method comprises transforming a plant cell with construct comprising a selected gene operably linked to a Coix promoter, and then regenerating a monocotyledonous plant which expresses the gene from the recipient cell. The method can be used to prevent gene silencing in a monocotyledonous plant. The methods can be used for transforming monocot plants such as rice, wheat, oats, barley, rye, sorghum and maize. They can be transformed with genes such as an insect resistance gene, a fungal disease resistance gene, a viral disease resistance gene, a bacterial disease resistance gene, a herbicide resistance gene, a gene affecting grain composition or quality, a nutrient utilization gene, a mycotoxin reduction gene, a male sterility gene, a selectable marker gene, a screenable marker gene, a negative selectable marker gene, a gene affecting plant agronomic characteristics, and an environment or stress resistance gene. The methods can also be used for producing transgenic dicot plants such as tobacco, tomato, potato, soybean and cotton.

SQ Sequence 31 BP; 7 A; 10 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 2.6%; Score 23; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGACCGGTTACGACACCACTG 23
AA245472/c
ID AA245472 standard; DNA; 29 BP.
XX
AC AA245472;
XX
DT 06-APR-2000 (first entry)
XX
DE PCR primer gcx-1pcr3'neo for the gamma-coixin gene promoter.

XX Gamma-coixin protein; monocotyledonous plant; Coix promoter;
KW gene silencing; rice; wheat; oat; barley; rye; sorghum; maize;
KW insect resistance; fungal disease resistance; viral disease resistance;
KW bacterial disease resistance; herbicide resistance; grain composition;
KW nutrient utilization; mycotoxin reduction; male sterility;
KW stress resistance; transgenic plant; PCR primer; ss.
XX
OS Coix lacryma-jobi.
XX
PN WO958659-A2.
XX
PD 18-NOV-1999.
XX
PP 14-MAY-1999; 99WO-US010776.
XX
PR 14-MAY-1998; 98US-00078972.
XX
PA (DEKA-) DEKALB GENETICS CORP.
XX
PI Kriz AL, Luethy MH, Voyles DA;
XX
DR WPI; 2000-126367/11.
XX
PT New isolated Coix regulatory sequences, used for producing transgenic plants with improved properties.
XX
PS Example 1; Page 153; 238pp; English.
XX
CC PCR primers AA245470-72 were used to amplify the promoter of the gamma-coixin gene for subsequent cloning. The promoter is used in the method of the invention. The specification describes a method of preparing a monocotyledonous plant (other than Coix sp.) expressing a selected gene. The method comprises transforming a plant cell with construct comprising a selected gene operably linked to a Coix promoter, and then regenerating

CC a monocotyledonous plant which expresses the gene from the recipient
 CC cell. The method can be used to prevent gene silencing in a
 CC monocotyledonous plant. The methods can be used for transforming monocot
 CC plants such as rice, wheat, oats, barley, rye, sorghum and maize. They
 CC can be transformed with genes such as an insect resistance gene, a fungal
 CC disease resistance gene, a viral disease resistance gene, a bacterial
 CC disease resistance gene, a herbicide resistance gene, a gene affecting
 CC grain composition or quality, a nutrient utilization gene, a mycotoxin
 CC reduction gene, a male sterility gene, a selectable marker gene, a
 CC selectable marker gene, a negative selectable marker gene, a gene
 CC affecting plant agronomic characteristics, and an environment or stress
 CC resistance gene. The methods can also be used for producing transgenic
 CC dicot plants such as tobacco, tomato, potato, soybean and cotton
 XX

SQ Sequence 29 BP; 2 A; 7 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 2.3%; Score 21; DB 3; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 874 AGAGCACGAAAGATCGACACC 894
 DB 29 AGAGCACGAAAGATCGACACC 9

RESULT 7
 AA245471/c
 ID AA245471 standard; DNA; 29 BP.
 AC
 XX AA245471;
 XX
 DT 06-APR-2000 (first entry)
 XX
 DE PCR primer gcc-1pcr3' xba for the gamma-coixin gene promoter.
 XX
 KM Gamma-coixin protein; monocotyledonous plant; Coix promoter;
 KM gene silencing; rice; wheat; oat; barley; rye; sorghum; maize;
 KM insect resistance; fungal disease resistance; viral disease resistance;
 KM bacterial disease resistance; herbicide resistance; grain composition;
 KM nutrient utilization; mycotoxin reduction; male sterility;
 KM stress resistance; transgenic plant; PCR primer; ss.
 XX
 OS Coix lacryma-jobi.
 XX
 PN WO9558659-A2.
 PD 18-NOV-1999.
 XX
 PF 14-MAY-1999; 99WO-US010776.
 XX
 PR 14-MAY-1998; 98US-00078972.
 XX
 PA (DEKA-) DEKALB GENETICS CORP.
 XX
 PI Kriz AL, Luethy MH, Voyles DA;
 DR WPI; 2000-126367/11.
 XX
 PT New isolated Coix regulatory sequences, used for producing transgenic
 PT plants with improved properties.
 XX
 PS Example 1; Page 153; 238pp; English.
 XX
 CC PCR primers AA245470-72 were used to amplify the promoter of the gamma-
 CC coixin gene for subsequent cloning. The promoter is used in the method of
 CC the invention. The specification describes a method of preparing a
 CC monocotyledonous plant (other than Coix sp.) expressing a selected gene.
 CC The method comprises transforming a plant cell with construct comprising
 CC a selected gene operably linked to a Coix promoter, and then regenerating
 CC a monocotyledonous plant which expresses the gene from the recipient
 CC cell. The method can be used to prevent gene silencing in a
 CC monocotyledonous plant. The methods can be used for transforming monocot
 CC plants such as rice, wheat, oats, barley, rye, sorghum and maize. They

CC can be transformed with genes such as an insect resistance gene, a fungal
 CC disease resistance gene, a viral disease resistance gene, a bacterial
 CC disease resistance gene, a herbicide resistance gene, a gene affecting
 CC grain composition or quality, a nutrient utilization gene, a mycotoxin
 CC reduction gene, a male sterility gene, a selectable marker gene, a
 CC selectable marker gene, a negative selectable marker gene, a gene
 CC affecting plant agronomic characteristics, and an environment or stress
 CC resistance gene. The methods can also be used for producing transgenic
 CC dicot plants such as tobacco, tomato, potato, soybean and cotton
 XX

SQ Sequence 29 BP; 3 A; 6 C; 9 G; 11 T; 0 U; 0 Other;

Query Match 2.3%; Score 21; DB 3; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 874 AGAGCACGAAAGATCGACACC 894
 DB 29 AGAGCACGAAAGATCGACACC 9

RESULT 8
 ABS54620
 ID ABS54620 standard; DNA; 32804 BP.
 XX
 AC ABS54620;
 XX
 DT 28-NOV-2002 (first entry)
 XX
 DE Human G protein-coupled receptor gene.
 XX
 KM Human; ds; gene; GPCR; G protein-coupled receptor; neuroleptic;
 KM antiparkinsonian; antiemetic; gastrointestinal;
 KM central nervous system disorder; schizophrenia; Parkinson's disease;
 KM migraine; vomiting induced by cancer therapy; gastric motility disorder;
 KM dopamine receptor; serotonin receptor.
 XX
 OS Homo sapiens.
 XX
 PN WO200263001-A2.
 PD 15-AUG-2002..
 XX
 PF 29-JAN-2002; 2002WO-US002151.
 XX
 PR 07-FEB-2001; 2001US-0266856P.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Beasley EM;
 DR WPI; 2002-706905/76.
 DR P-PSDB; ABG70854.
 XX
 PT New isolated human G protein-coupled receptor (GPCR) peptides, useful for
 PT developing therapeutic and diagnostic compositions for diagnosing or
 PT treating a disease mediated by a GPCR protein.
 XX
 PS Claim 4; Page 57-71; 72pp; English.
 XX
 CC The invention relates to a new isolated peptide comprising a human G
 CC protein-coupled receptor (GPCR) appearing as ABG70854, its fragment
 CC (comprising at least 10 contiguous amino acids), orthologue or allelic
 CC variant, encoded by a nucleic acid molecule that hybridises to the
 CC opposite strand of a nucleic acid molecule appearing as ABS54620 (the
 CC gene) or ABS54621 (partial cDNA). Also included are an isolated antibody
 CC that selectively binds to the GPCR, a gene chip comprising the nucleic
 CC acids, a transgenic non-human animal, a nucleic acid vector, a host cell,
 CC and identifying modulators/binding agents of the GPCR or nucleic acid.
 CC The GPCR peptides, proteins, nucleic acid molecules and agents are useful
 CC for the development of human therapeutic targets, to aid in the
 CC identification of therapeutic proteins, and to serve as targets for the
 CC development of human therapeutic agents. The peptide may be used in drug

CC screening assays, in assays to determine the biological activity of the
CC protein, to raise antibodies or to elicit another immune response, as a
CC reagent in assays designed to quantitatively determine levels of the
CC protein in biological fluids, or as markers for tissues in which the
CC corresponding protein is preferentially expressed. The GPCR peptides are
CC also useful for diagnosing a disease, predisposition to a disease, or
CC treating a disorder characterized by an absence of, inappropriate or
CC unwanted expression of the protein. These disorders include central
CC nervous system disorders such as schizophrenia, Parkinson's disease,
CC migraine, vomiting induced by cancer therapy and gastric motility
CC disorders resulting from an alteration in function of dopamine and
CC serotonin receptors. The antibodies are useful in pharmacogenomic
CC analysis, for inhibiting protein function, or for tissue typing. The
CC nucleic acid molecules are useful as probes, primers, chemical
CC intermediates, as antisense constructs to control GPCR gene expression,
CC or in biological assays. The present sequence is the GPCR gene
XX
SQ Sequence 32804 BP; 9106 A; 5820 C; 6310 G; 11568 T; 0 U; 0 Other;

Query Match 2.2%; Score 20; DB 6; Length 32804;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 699 TCGATGAGTCATAAATATTG 718
DB 8044 TCGATGAGTCATAAATATTG 8063

RESULT 9
ABO69245_15
Continuation (16 of 31) of ABO69245 from base 1500001 (Listeria innocua DNA sequence #68
WP Sequence split into 31 fragments LOCUS ABO69245 Accession ABO69245

WP	Fragment Name	Begin	End
WP	ABO69245_00	1	110000
WP	ABO69245_01	100001	210000
WP	ABO69245_02	200001	310000
WP	ABO69245_03	300001	410000
WP	ABO69245_04	400001	510000
WP	ABO69245_05	500001	610000
WP	ABO69245_06	600001	710000
WP	ABO69245_07	700001	810000
WP	ABO69245_08	800001	910000
WP	ABO69245_09	900001	1010000
WP	ABO69245_10	1000001	1110000
WP	ABO69245_11	1100001	1210000
WP	ABO69245_12	1200001	1310000
WP	ABO69245_13	1300001	1410000
WP	ABO69245_14	1400001	1510000
WP	ABO69245_15	1500001	1610000
WP	ABO69245_16	1600001	1710000
WP	ABO69245_17	1700001	1810000
WP	ABO69245_18	1800001	1910000
WP	ABO69245_19	1900001	2010000
WP	ABO69245_20	2000001	2110000
WP	ABO69245_21	2100001	2210000
WP	ABO69245_22	2200001	2310000
WP	ABO69245_23	2300001	2410000
WP	ABO69245_24	2400001	2510000
WP	ABO69245_25	2500001	2610000
WP	ABO69245_26	2600001	2710000
WP	ABO69245_27	2700001	2810000
WP	ABO69245_28	2800001	2910000
WP	ABO69245_29	2900001	3010000
WP	ABO69245_30	3000001	311208

Query Match 2.2%; Score 20; DB 6; Length 110000;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 468 TTCATGAAAAAACAAATTAAG 487
DB 98605 TTCATGAAAAAACAAATTAAG 98624

RESULT 10
ABO67195_1/C
Continuation (2 of 5) of ABO67195 from base 100001 (Listeria innocua contig DNA sequence
WP Sequence split into 5 fragments LOCUS ABO67195 Accession ABO67195

WP	Fragment Name	Begin	End
WP	ABO67195_0	1	110000
WP	ABO67195_1	100001	210000
WP	ABO67195_2	200001	310000
WP	ABO67195_3	300001	410000
WP	ABO67195_4	400001	495269

Query Match 2.2%; Score 20; DB 6; Length 110000;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 468 TTCATGAAAAAACAAATTAAG 487
DB 60350 TTCATGAAAAAACAAATTAAG 60331

RESULT 11
ADL10270
ID ADL10270 standard; cDNA; 334 BP.
XX
AC ADL10270;
XX
DT 01-JUL-2004 (first entry)

XX Cat flea hindgut and malpighian tubule (HMT) protein cDNA #687.

XX Flea; head and nerve cord protein; HNC;
KW hindgut and malpighian tubule protein; HMT; flea infestation;
KW anti-arthropod vaccine; chemotherapeutic drug; insecticide; gene; ss;
KW cat flea.

XX Ctenocephalides felis.

XX US2004067516-A1.

XX 08-APR-2004.

XX 16-JUL-2003; 2003US-00621901.

XX 22-JUL-2002; 2002US-0319414P.

XX (BRAN/) BRANDT K S.

XX (GAIN/) GAINES P J.

XX (STIN/) STINCHCOMB D T.

XX (WISN/) WISNEWSKI N.

XX Brandt KS, Gaines PJ, Stinchcomb DT, Wisniewski N;

XX WPI; 2004-304579/28.

XX Novel flea head and nerve cord protein and flea hindgut and malpighian

XX tubule protein, useful for reducing flea infestations.

XX Claim 5; SEQ ID NO 707; 35bp; English.

CC The invention relates to a flea head and nerve cord (HNC) protein and a
CC flea hindgut and malpighian tubule (HMT) protein. The invention also
CC relates to an isolated nucleic acid molecule expressed by a tissue chosen
CC from a flea HMT tissue and a flea HNC tissue, identified by a method
CC involving constructing a cDNA library enriched for HMT or HNC expressed
CC sequences and identifying a nucleic acid molecule in the library, and an
CC isolated antibody that selectively binds an HNC or HMT protein. The
CC proteins are useful for identifying compounds capable of inhibiting
CC activity of the proteins which involves contacting a protein with a
CC putative inhibitory compound under conditions in which, in the absence of
CC the compound, the protein has activity, and determining if the putative
CC inhibitory compound inhibits its activity. The proteins, nucleic acids
CC and antibodies are useful for reducing flea infestations. The proteins

CC and nucleic acids are useful as targets for anti-arthropod vaccines and
 CC chemotherapeutic drugs. The proteins are useful for producing a
 CC recombinant protein vaccine to protect an animal from flea infestation.
 CC The antibodies are useful for passively immunising an animal in order to
 CC protect the animal from fleas, as tools to screen expression libraries
 CC and/or for recovering desired proteins from a mixture of proteins and
 CC other contaminants. The antibodies are also useful for targeting
 CC cytotoxic agents to fleas in order to directly kill such fleas. This
 CC sequence represents cDNA encoding a cat flea HMT protein of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification but was obtained in electronic format directly
 CC from USPTO at seqdata.uspto.gov/sequence.html.
 CC
 SQ Sequence 334 BP; 126 A; 57 C; 37 G; 107 T; 0 U; 7 Other;
 Query Match 2.1%; Score 19; DB 12; Length 334;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 298 TCACAAATGCGAGTCAA 316
 Db 20 TCACAAATGCGAGTCAA 38
 RESULT 12
 AB253324
 ID AB253324 standard; cDNA; 400 BP.
 AC AB253324;
 XX
 DT 28-MAR-2003 (first entry)
 XX
 DE Aspergillus oryzae polynucleotide SEQ ID NO 2437.
 XX
 KM Aspergillus oryzae; fermentation; fungus; industrial; EST;
 KM expressed sequence tag; gene; ss.
 XX
 OS Aspergillus oryzae.
 PN WO200279476-A1.
 XX
 PD 10-OCT-2002.
 PF 22-MAR-2002; 2002WO-IB000890.
 PR 30-MAR-2001; 2001JP-00098371.
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (NARE-) NAT RES INST BREWING.
 PA (NORQ) NAT FOOD RES INST MIN AGRIC.
 XX
 PI Machida M, Akita O, Kashiwagi Y, Kitamoto K, Horiuchi H;
 PI Takeuchi M, Kobayashi T, Kitamoto N, Gomi K, Abe K;
 XX
 DR WPI; 2003-046817/04.
 PT Detection of expression of specific Aspergillus genes for monitoring the
 PT fermentation and growth conditions of the fungus, using DNA probes.
 XX
 PS Claim 1; SEQ ID NO 2437; 48pp + Sequence listing; Japanese.
 XX
 CC The invention relates to a polynucleotide having any of 6006 specific
 CC sequences (AB253888-AB258931), which are expressed by a fungus under
 CC specific culture conditions including one or more of eutrophic,
 CC oligotrophic, solid, early germination, alkaline, high temperature, low
 CC temperature or maltose culture or polynucleotides stringently hybridising
 CC to these sequences. The polynucleotides are useful for monitoring the
 CC progress of fermentation and the growth conditions of a fungus,
 CC especially of Aspergillus oryzae which is widely used in industrial
 CC fermentation. Also monitoring for fungal contamination. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 400 BP; 80 A; 151 C; 89 G; 80 T; 0 U; 0 Other;
 Query Match 2.1%; Score 19; DB 8; Length 400;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 733 AAGCTACACAGCCGTGTC 751
 Db 154 AAGCTACACAGCCGTGTC 172
 RESULT 13
 AA112219/C
 ID AA112219 standard; DNA; 497 BP.
 AC AA112219;
 XX
 DT 12-OCT-2001 (first entry)
 XX
 DE Probe #2152 for gene expression analysis in human cervical cell sample.
 XX
 KM Probe; human; microarray; gene expression; cervical epithelial cell;
 KM cervical cancer; ss.
 XX
 OS Homo sapiens.
 PN WO200157278-A2.
 XX
 PD 09-AUG-2001.
 PF 30-JAN-2001; 2001WO-US000670.
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488901/53.
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human cervical epithelial cells.
 XX
 PS Claim 25; SEQ ID NO 2152; 487pp; English.
 XX
 CC The present invention relates to human single exon nucleic acid probes
 CC (SENPs). The present sequence is one such probe. The SENPs are derived
 CC from human HeLa cells. The SENPs can be used to produce a single exon
 CC microarray, which can be used for measuring human gene expression in a
 CC sample derived from human cervical epithelial cells. By measuring gene
 CC expression, the probes are therefore useful in grading and/or staging of
 CC diseases of the cervix, notably cervical cancer. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 497 BP; 145 A; 105 C; 141 G; 106 T; 0 U; 0 Other;
 Query Match 2.1%; Score 19; DB 4; Length 497;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 338 CGTCTCCTTGAGCTGTA 356
 Db 181 CGTCTCCTTGAGCTGTA 163

```

RESULT 14
AI133573/C
ID AI133573 standard; DNA; 497 BP.
XX
AC AI133573;
XX
DT 17-OCT-2001 (first entry)
XX
DE Probe #2259 used to measure gene expression in human placenta sample.
XX
KM Probe; microarray; human; placenta; antenatal diagnosis;
XX
KW Genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
PS Claim 25; SEQ ID NO 2259; 654bp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders
XX
SQ Sequence 497 BP; 145 A; 105 C; 141 G; 106 T; 0 U; 0 Other;
Query Match 2.1%; Score 19; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 338 CGTCTCCTGTGAGCTTGTA 356
DB 181 CGTCTCCTGTGAGCTTGTA 163

```

```

PN WO200157271-A2.
PD 09-AUG-2001.
XX
AC 30-JAN-2001; 2001WO-US000662.
XX
PF 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-496933/54.
XX
PT New spatially-addressable set of single exon nucleic acid probes, useful
PT for measuring gene expression in sample derived from human breast,
PT comprises number of single exon nucleic acid probes.
XX
PS Claim 1; SEQ ID NO 2168; 327bp + Sequence Listing; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting the
CC probes with a collection of detectably labelled nucleic acids derived
CC from mRNA of human breast, and then measuring the label bound to each
CC probe of the microarray. The probes are useful for verifying the
CC expression of regions of genomic DNA predicted to encode proteins. They
CC are useful for gene discovery, and for determining predisposition and/or
CC prognosing breast disease. Gene expression analysis is useful for
CC assessing the toxicity of chemical agents on cells. The microarray of
CC this invention presents a far greater diversity of probes for measuring
CC gene expression, with far less bias than expressed sequence tag
CC microarrays. The method is suitable for rapid production of functional
CC information from genomic sequence. The present sequence is a single exon
CC nucleic acid probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 497 BP; 145 A; 105 C; 141 G; 106 T; 0 U; 0 Other;
Query Match 2.1%; Score 19; DB 4; Length 497;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 338 CGTCTCCTGTGAGCTTGTA 356
DB 181 CGTCTCCTGTGAGCTTGTA 163

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Search completed: September 24, 2005, 17:26:58
Job time : 548 secs

size-selected to contain the 0.5-3 kb size fraction."

ORIGIN

Query Match 2.5%; Score 22; DB 7; Length 580;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 458 CAAAGTTGTTTCATGAAAAA 479
|||||
Db 534 CAAAGTTGTTTCATGAAAAA 555

RESULT 2
CC433166 402 bp DNA linear GSS 20-MAY-2003
DEFINITION PUDG777TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMB1210M09,
genomic survey sequence.
ACCESSION CC433166
VERSION CC433166.1 GI:30928694
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 402)
WhiteLaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
Resnick,A., Fraiser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
Maize Genomics Consortium
Unpublished (2003)
Contact: Cathy WhiteLaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whiteLaw@cigr.org
Seq primer: TP
Class: sheared ends.

FEATURES
Location/Qualifiers
1..402
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="873"
/db_xref="taxon:4577"
/clone="ZMMB1210M09"
/clone_1db="ZM_0.6_1.0_KB"
/note="vector: PCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"

ORIGIN

Query Match 2.3%; Score 21; DB 8; Length 402;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 72 AATCACCCTGTCTGTCTACAA 92
|||||
Db 13 AATCACCCTGTCTGTCTACAA 33

RESULT 3
B2349555 418 bp DNA linear GSS 12-NOV-2002
LOCUS B2349555
DEFINITION hr42b09.g1 WGS-Sbicolorf (JM107 adapted methyl filtered) Sorghum
bicolor genomic clone hr42b09 5', genomic survey sequence.
ACCESSION B2349555
VERSION B2349555.1 GI:24911703
KEYWORDS GSS.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Sorghum.

REFERENCE
AUTHORS 1 (bases 1 to 418)
Rabinowicz,P.D., O'Shaughnessy,A.L., Ballja,V., Dedhia,N.,
Katzemburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
Zutavern,F., Palmer,L., McCombie,W.R. and Marienissen,R.A.
Genomic shotgun sequences from Sorghum bicolor (methyl-filtered)
Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Plate: hr42 row: b column: 09
Seq primer: -21M13uniRev
Class: shotgun
High quality sequence stop: 418.

FEATURES
Location/Qualifiers
1..418
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/db_xref="taxon:4558"
/clone="hr42b09"
/lab_host="JM107 or DH5a"
/clone_1db="WGS-Sbicolorf (JM107 adapted methyl filtered)"
/note="Site 1: Xba I; Site 2: Xba I; The vector was
digested with Xba I and one nucleotide was added by fill in
in the recessive 3' end. The genomic DNA was nubilized,
end repaired, adaptor ligated and size fractionated using
sephadex. The resulting fragments were between 0.8 and 3
kb and were cloned into the vector (x/y reads in M13mp19,
b/g reads in pUC19). The same ligation was transformed in
either JM107 or DH5a."

ORIGIN

Query Match 2.3%; Score 21; DB 8; Length 418;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 686 TACATTAAGTGAATGATGACT 706
|||||
Db 236 TACATTAAGTGAATGATGACT 256

RESULT 4
CL553734/c 602 bp DNA linear GSS 14-JUN-2004
LOCUS CL553734
DEFINITION OB_Ba0002A14.f OB_Ba Oryza brachyantha genomic clone
OB_Ba0002A14 5', genomic survey sequence.
ACCESSION CL553734
VERSION CL553734.1 GI:47630602
KEYWORDS GSS.
SOURCE Oryza brachyantha
ORGANISM Oryza brachyantha
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoidae; Oryzaceae; Oryza.
1 (bases 1 to 602)
Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jerry,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
OMAP Project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 145000 Std Error: 0.00

Plate: 0002 row: A column: 14
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends

FEATURES

Location/Qualifiers

1..602
/organism="Oryza brachyantha"
/mol_type="genomic DNA"
/db_xref="taxon:4533"
/clone="OB_BA0002A14"
/cissue_type="leaves"
/dev_stage="mature"
/lab_host="DH10B"
/clone_lid="OB_Ba"
/note="Vector: pGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN

Query Match 2.3%; Score 21; DB 9; Length 602;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 463 TTTCCTTCATGAAAAACAAA 483
|||||
Db 250 TTTCCTTCATGAAAAACAAA 230

RESULT 5

CL029329

LOCUS CL029329 961 bp DNA linear GSS 31-DEC-2003
DEFINITION CH216-28M20_Sp6.1 CH216 Xenopus tropicalis genomic clone
ACCESSION CL029329
VERSION CL029329.1 GI:40475916
KEYWORDS GSS.

SOURCE

ORGANISM

Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

REFERENCE

AUTHORS

1 (bases 1 to 961)
Kremetzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E. and Wilson, R.

TITLE

A physical map of the xenopus tropicalis genome
Unpublished (2003)

JOURNAL

COMMENT

Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp6 ATTAGGTGACACTATAG
Class: BAC ends
High quality sequence start: 24
High quality sequence stop: 790.
Location/Qualifiers

FEATURES

source

1..961
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-28M20"
/sex="male"
/cell_line="Strock 248 F7A2, inbred N7"
/clone_lid="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"

ORIGIN

Query Match 2.3%; Score 21; DB 9; Length 961;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 527 GTGAATTTACAAAGCCATATA 547
|||||
Db 197 GTGAATTTACAAAGCCATATA 217

RESULT 6

CNS041WG/c

LOCUS

CNS041WG 1009 bp DNA linear GSS 01-SEP-2000
Tetraodon nigroviridis genome survey sequence T7 end of clone
113G04 of library G from Tetraodon nigroviridis, genomic survey
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

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AUTHORS

TITLE

J

ORGANISM Meloidogyne arenaria
 Eukaryote; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogynae.
 1 (bases 1 to 308)
 McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucba, T., Theising, B., Bowers, Y., Gibbons, M., Ritzer, E., Bennett, J., Franklin, C., Traagereihvill, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
 The Washington Univ. Nematode EST Project, 1999
 Unpublished (1999)
 Contact: McCarter JP
 The Washington Univ. Nematode EST Project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 Cloned unidirectionally. Poly(A)⁺ RNA was concentrated and purified using Dynabeads (Dyna) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5' SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information.
 Putative full length read
 The vector to vector length is 326
 Seq primer: -40RP from Gibco.
 Location/Qualifiers
 1..308
 /organism="Meloidogyne arenaria"
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 /db_xref="taxon:6304"
 /feature_type="whole organism"
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 /lab_host="DH10B"
 /clone_lib="Meloidogyne arenaria J2 SMART pGEM"
 /note="Vector: plasmid (ampicillin resistant); Site 1: XhoI; Site 2: NotI; Cloned unidirectionally. Poly(A)⁺ RNA was concentrated and purified using Dynabeads (Dyna) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5' SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractionated on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information."

ORIGIN

Query Match 2.2%; Score 20; DB 7; Length 308;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 459 AAAGTTGTTTCATGAAAAA 478
 ||||||||||||||||||||
 Db 41 AAAGTTGTTTCATGAAAAA 22

RESULT 8
 AA372261

LOCUS AA372261 395 bp RNA linear EST 21-Apr-1997
 DEFINITION EST84398 Colon adenocarcinoma IV Homo sapiens cDNA 5' end similar to EST containing Alu repeat. mRNA sequence.
 ACCESSION AA372261
 VERSION AA372261.1 GI:2024812
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 395)
 Adams, M.D., Kexlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bull, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Men-Hai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghegan, N.S., Glodde, A., Gnehm, C.L., Hanna, M.C., Heddlom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Sauder, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Uterback, T.R., Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrite, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.
 Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
 Nature 377 (6547 Suppl), 3-174 (1995)
 MEDLINE 96026280
 PUBMED 7566098
 COMMENT Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlavage@igrr.org
 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/cdb/hgi/hgi.html>)
 Seq primer: M13 Reverse.
 Location/Qualifiers
 1..395
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 /mol_type="mRNA"
 /db_xref="ATCC (Inhost):176850"
 /db_xref="taxon:9606"
 /dev_stage="adult"
 /clone_lib="Colon adenocarcinoma IV"
 /note="Organ: colon; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI"

ORIGIN

Query Match 2.2%; Score 20; DB 1; Length 395;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 86 TCTACAGACGAGCAATG 105
 ||||||||||||||||||||
 Db 22 TCTACAGACGAGCAATG 41

RESULT 9
 H01412 411 bp RNA linear EST 19-JUN-1995
 LOCUS H01412
 DEFINITION y139c09.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147376 5', mRNA sequence.
 ACCESSION H01412
 VERSION H01412.1 GI:864345
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 411)

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, J., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P., and Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

FEATURES High quality sequence stops: 331
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 565 Std Error: 0.00
Seq primer: M13RP1

Location/Qualifiers
High quality sequence stop: 331.
1. .411
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:559022"
/db_xref="taxon:9606"
/clone="IMAGE:147376"
/sex="Female"
/dev_stage="placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares placenta M2HP"
/note="Organ: placenta; Vector: p773D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' ACTGGAAGATTCGCGCGCAGCAATTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p773 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bernaldo. "

ORIGIN

Query Match 2.2%; Score 20; DB 7; Length 411;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 129 CGTCTCTGACGTCTTTC 148
|||||
Db 137 CGTCTCTGACGTCTTTC 156

RESULT 10
BM130557 436 bp mRNA linear EST 27-NOV-2001
LOCUS BM130557
DEFINITION p106d08.y1 Ancylostoma ceylanicum M1 S11 TOPO Kapulkin Ancylostoma ceylanicum cDNA 5' similar to TR:Q22288 Q22288 T07C4.5 PROTEIN. [1]
; mRNA sequence.
ACCESSION BM130557
VERSION BM130557.1 GI:17125109
KEYWORDS EST.
SOURCE Ancylostoma ceylanicum
ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida; Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma. 1 (bases 1 to 436)
REFERENCE McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,

TITLE Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagarishevili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Sailer, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.

JOURNAL The Washington Univ. Nematode EST Project, 1999

COMMENT Unpublished (1999)
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

FEATURES The library was constructed by Dr. Vadim Kapulkin from the University of Colorado at Boulder. DNA Sequencing by: Washington University Genome Sequencing Center
Seq primer: S11 primer.

Location/Qualifiers
1. .436
/organism="Ancylostoma ceylanicum"
/mol_type="mRNA"
/db_xref="taxon:53326"
/sex="mixed"
/dev_stage="adults"
/lab_host="DH10B"
/clone_lib="Ancylostoma ceylanicum M1 S11 TOPO Kapulkin"
/note="Vector: PCR-XL-TOPO (Invitrogen); Site 1: EcoRI; Site 2: EcoRI; S11 PCR-based library. Ancylostoma ceylanicum cDNA PCR products of size nucleotides containing S11 on the 5' end and oligo(dT) on the 3' end were non-directionally cloned into PCR-XL-TOPO (Invitrogen) following the cloning protocol. The cDNA insert can be excised by digestion with EcoRI. The library was constructed by Dr. Vadim Kapulkin from the University of Colorado at Boulder."

ORIGIN

Query Match 2.2%; Score 20; DB 4; Length 436;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 632 CCACGCAAAATGCAATG 651
|||||
Db 22 CCACGCAAAATGCAATG 41

RESULT 11
BT04715 440 bp mRNA linear EST 18-SEP-2001
LOCUS BT04715
DEFINITION p102f11.y1 Ancylostoma ceylanicum M1 S11 TOPO Kapulkin Ancylostoma ceylanicum cDNA 5' similar to TR:Q22288 Q22288 T07C4.5 PROTEIN. [1]
; mRNA sequence.
ACCESSION BT04715
VERSION BT04715.1 GI:15666933
KEYWORDS EST.
SOURCE Ancylostoma ceylanicum
ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida; Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma. 1 (bases 1 to 440)
REFERENCE McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagarishevili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Sailer, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.

TITLE The Washington Univ. Nematode EST Project, 1999

JOURNAL Unpublished (1999)

COMMENT Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 The library was constructed by Dr. Vadim Kapulkin from the University of Colorado at Boulder. DNA Sequencing by: Washington University Genome Sequencing Center
 Seq primer: SL1 primer
 Location/Qualifiers

FEATURES
 Source

1..440
 /organism="Ancylostoma ceylanicum"
 /mol_type="mRNA"
 /db_xref="taxon:53326"
 /sex="mixed"
 /dev_stage="adults"
 /lab_host="DHI08"
 /clone_lib="Ancylostoma ceylanicum M1 SL1 TOPO Kapulkin"
 /note="Vector: PCR-XL-TOPO (Invitrogen); Site 1: EcoRI; Site 2: EcoRI; SL1 PCR-based library. Ancylostoma ceylanicum cDNA PCR products of size nucleotides containing SL1 on the 5' end and oligo(dT) on the 3' end were non-directionally cloned into PCR-XL-TOPO (Invitrogen) following the cloning protocol. The cDNA insert can be excised by digestion with EcoRI. The library was constructed by Dr. Vadim Kapulkin from the University of Colorado at Boulder."

ORIGIN

Query Match 2.2%; Score 20; DB 4; Length 440;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 632 CCACGCAAAATGCAGATG 651
 |||||
 DB 20 CCACGCAAAATGCAGATG 39

RESULT 12
 CBI75122 491 bp mRNA linear EST 31-JAN-2003
 LOCUS pR80b08.y1 Ancylostoma ceylanicum L3 Ancylostoma ceylanicum cDNA 5'
 DEFINITION similar to TR:Q22288 Q22288 T07C4.5 PROTEIN. [1] ;, mRNA sequence.
 CBI75122
 CBI75122.1 GI:28184012
 EST.
 SOURCE Ancylostoma ceylanicum
 ORGANISM Ancylostoma ceylanicum
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida; Ancylostomatidae; Ancylostomatidae; Ancylostomatidae; Ancylostoma.
 1 (bases 1 to 491)
 McCarter,J., Clifton,S., Chiapelli,B., Page,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucada,T., Theising,B., Bowers,Y., Gibbons,M., Ritzer,E., Bennett,J., Franklin,C., Tsagaris,I., R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Waller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McMan,R., Waterston,R. and Wilson,R.,
 The Washington Univ. Nematode EST Project, 1999
 Unpublished (1999)
 Contact: McCarter JP
 The Washington Univ. Nematode EST Project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Lambda ZAP II library (99% recombinants, average insert size 1500bp, amplified one time (106 pfu) donated by John Hawdon of The George Washington University, Washington DC(mcmjmg@umc.edu).
 Claire Murphy and Dr. James McCarter of Washington University GSC, St. Louis, MO mass excised the plasmid from the Lambda ZAP II library.
 Seq primer: T3 from Gibco.

FEATURES

Source

Location/Qualifiers
 1..491
 /organism="Ancylostoma ceylanicum"
 /mol_type="mRNA"
 /db_xref="taxon:53326"
 /dev_stage="infective third larval stage (L3)"
 /lab_host="SOLR (Stratagene)"
 /clone_lib="Ancylostoma ceylanicum L3"
 /note="Vector: pBluescript SK + excised from Lambda ZAP II (Stratagene); Site 1: XhoI; Site 2: EcoRI; Lambda ZAP II Library (99% recombinants, average insert size 1500bp, amplified one time (106 pfu) donated by John Hawdon of The George Washington University, Washington DC (mcmjmg@umc.edu). Claire Murphy and Dr. James McCarter of Washington University GSC, St. Louis, MO mass excised the plasmid from the Lambda ZAP II library."

ORIGIN

Query Match 2.2%; Score 20; DB 6; Length 491;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 632 CCACGCAAAATGCAGATG 651
 |||||
 DB 71 CCACGCAAAATGCAGATG 90

RESULT 13
 AA555428 576 bp mRNA linear EST 23-AUG-2000
 LOCUS CBEEST.660 unizAPCp10WAp001lib3 Cryptosporidium parvum cDNA 5',
 DEFINITION mRNA sequence.
 AA555428
 AA555428.1 GI:2325967
 EST.
 SOURCE Cryptosporidium parvum
 ORGANISM Cryptosporidium parvum
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Cryptosporididae; Cryptosporidium.
 1 (bases 1 to 576)
 Strong,W.B. and Nelson,R.G.
 Preliminary profile of the Cryptosporidium parvum genome: an expressed sequence tag and genome survey sequence analysis
 Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)
 MEDLINE 20183851
 PUBMED 10717289
 Contact: Nelson, R. G.
 Depts. of Medicine & Pharmaceutical Chemistry
 San Francisco General Hospital-University of California, San Francisco
 Box 0811, San Francisco, CA 94143-0811, USA
 Tel.: 415 206 8846
 Fax: 415 206 3353
 Email: malari@itsa.ucsf.edu
 Submitted sequence has been edited to remove vector sequences 5' to the insert, to correct miscalled bases and assign uncalled (N) bases throughout the sequence, and to terminate when base-calling became ambiguous.
 Seq primer: M13 reverse
 High quality sequence stop: 576.
 Location/Qualifiers

FEATURES

Source

1..576
 /organism="Cryptosporidium parvum"
 /mol_type="mRNA"
 /strain="IOWA"
 /db_xref="taxon:5807"
 /dev_stage="sporozoite"
 /lab_host="E. coli XL1 Blue MRF⁺ Kan"
 /clone_lib="unizAPCp10WAp001lib3"
 /note="Vector: unizAP XR; Site 1: EcoRI; Site 2: Xho I; The C. parvum cDNA library was prepared by Drs. Norman J. Pieniazek, Michael J. Arrowood, Susan B. Slomenda, and Jan R. Mead at the Centers for Disease Control and Prevention

/note=Site: Sali; Site 2 BamII; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genetic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGAGAGCTTCAGAGCTTTTTTTTTTAA 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length b cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 459.0. Second

strand cDNA was prepared with the primer adapter of
sequence 5' GAGAGAGAGATTCTCGAGTAAATTAATCCCCCCCCC
3'. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC 1."

ORIGIN

Query Match 2.2%; Score 20; DB 2; Length 621;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 811 TATGCACTTCTCATCACCA 830
|||||
Db 444 TATGCACTTCTCATCACCA 425

Search completed: September 24, 2005, 19:24:39
Job time : 3131 secs

D	b		301	CAAAATTGACAGTCAATGGATTGGGTGAGAAACAATACTCCTTCCTTGAGTTGCATCAAT	360
O	y		361	GAACTGATGTGATCATGATGATCACACTGATCCGATCTGATATATATGCCAATAGCTCA	420
D	b		361	GAAAGGAATGGTAGAGTCATGAGTCAACACTGATCCGATCTGATATATATGCGCAATAGCTCA	420
O	y		421	CACGCAACATTTACAAAACAACCCCATCTACTATCATCACAAAGTTSTTTTCATGAAAAAAC	480
D	b		421	CACGCAACATTTACAAAACAACCCCATCTACTATCATCATCAAAGTTTGTTCATGAAAAAAC	480
O	y		481	AAATTAAGTATGCAGGAGGGGACAATTAATCTTTGCTTGAACGCGTAAAGTAAATTTACAAAG	540
D	b		481	AAATTAAGTATGCAGGAGGGGACAATTAATCTTTGCTTGAACGCGTAAAGTAAATTTACAAAG	540
O	y		541	CCATATATCAACCCTATATCTTAATTAAATGAATTCCTTATATATATGCAAGATATCATCA	600
D	b		541	CCATATATCAACCCTATATCTTAATTAAATGAATTCCTTATATATATGCAAGATATCATCA	600
O	y		601	CAACCGTACTGTGTAAGAAGCAACAATAATGAGCCAGCAAAAAATGCAGAAATGAATCATAT	660
D	b		601	CAACCGTACTGTGTAAGAAGCAACAATAATGAGCCAGCAAAAAATGCAGAAATGAATCATAT	660
O	y		661	GATGACGAACGTACACATCGGCTTGCTACTATAAAGTGAATGATGAGTCATTAATATTTGGC	720
D	b		661	GATGACGAACGTACACATCGGCTTGCTACTATAAAGTGAATGATGAGTCATTAATATTTGGC	720
O	y		721	AAGAAACCGTGAAACCTACACAGCCGTGCTCAGTAGACCAAGAAACAAGAAACATGTCCT	780
D	b		721	AAGAAACCGTGAAACCTACACAGCCGTGCTCAGTAGACCAAGAAACAAGAAACATGTCCT	780
O	y		781	AATGCAACCTATAAATAACCCCTAGTAGCTCTATGCACTTCTCCATCAGCACTACCCATAT	840
D	b		781	AATGCAACCTATAAATAACCCCTAGTAGCTCTATGCACTTCTCCATCAGCACTACCCATAT	840
O	y		841	CTTCAGTCTATTACCTTCTCTATCTTATCTTACGAGAGGACACAGAAGATCGACACC	894
D	b		841	CTTCAGTCTATTACCTTCTCTATCTTATCTTACGAGAGGACACAGAAGATCGACACC	894
RESULT 2					
US-09-078-972A--19					
Sequence 19, Application US/09078972A					
Patent No. 6635806					
GENERAL INFORMATION:					
APPLICANT: KRIS, ALAN L.					
APPLICANT: LUETHY, MICHAEL H.					
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EXPRESSION OF TRANSGENES					
FILE REFERENCE: DEKM:158					
CURRENT APPLICATION NUMBER: US/09/078,972A					
CURRENT FILING DATE: 1998-05-14					
NUMBER OF SEQ ID NOS: 28					
SOFTWARE: PatentIn Ver. 2.0					
SEQ ID NO 19					
LENGTH: 412					
TYPE: DNA					
ORGANISM: Artificial Sequence					
FEATURE:					
OTHER INFORMATION: Description of Artificial Sequence: Synthetic					
US-09-078-972A--19					

	Query March	46.0%;	Score 411;	DB 4;	Length 412;
	Best Local Similarity	100.0%;	Pred. No. 4e-203;		
	Matches 411;	Conservative	0;	Mismatches	0; Indels 0; Gaps 0
QY	484	TAAGTATCAGAGGGGCA	CAATATATCTTGGCTTGA	CGCTAAGTGAATTTCAAA	GCCA 543
Db	2	TAAGTATCAGAGGGGCA	CAATATATCTTGGCTTGA	CGCTAAGTGAATTTCAAA	GCCA 61
OY	544	TATATCAACCTATATCTA	TATATTAAGTTGTTATATAT	AGCAGATGATCATCA	CAA 603

Db	62	TATATCAACCTATATCTATTAATTAATAGTTGGTTATATATATACGACGATGATCATCAACAA	121
Qy	604	CCGTACCTGTGAAAGGCACAAAATGACCACGCAAAAATGCACAATGAATCCATATGAT	663
Db	122	CGGTACTCTGTGAAGGCAACAAATGACACGCAAAAATGCACAATGAATCCATATGAT	181
Qy	664	GACGAACGTACACTCGGCTTGGTCTACATTAAGTATGATGATGATCAATTAATTTGGCAAG	723
Db	182	GACGAACGTACACTCGGCTTGGTCTACATTAAGTATGATGATGATCAATTAATTTGGCAAG	241
Qy	724	AAACCGTGAACGTCACACGCGCTGTATGATGACACAGGAACACAAAGAACTGTGCTAAT	783
Db	242	AAACCGTGAACGTCACACGCGCTGTATGATGACACAGGAACACAAAGAACTGTGCTAAT	301
Qy	784	CGAAGCTATAAATTAACCCCTAGTATGCTCATCTTCATCAACCACTACCATATCTT	843
Db	302	CGAAGCTATAAATTAACCCCTAGTATGCTCATCTTCATCAACCACTACCATATCTT	361
Qy	844	CAGTCATTTACCTTCTCTATCTACTCCAGAGAGACAGAAAGATCGACACC	894
Db	362	CAGTCATTTACCTTCTCTATCTACTCCAGAGAGACAGAAAGATCGACACC	412

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RESULT 3
US-09-078-972A-18
; Sequence 18: Application US/09078972A
; Patent No. 6635806
; GENERAL INFORMATION:
; APPLICANT: KRIS, ALAN L.
; APPLICANT: LOETHY, MICHAEL H.
; APPLICANT: VOYLES, DALE A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EXPRESSION OF TRANSGENES
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: DEKM:158
; CURRENT APPLICATION NUMBER: US/09/078,972A
; CURRENT FILING DATE: 1998-05-14
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 222
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-078-972A-18

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Query Match	24.7%	Score 221	DB 4	Length 222	
Best Local Similarity	100.0%	Pred. No. 1.7e-104			
Matches 221	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
QY	674	CACTCGGCTTCTCATTAAGTGAATGATGATCAATAATTTGGCAGAAGACCGTGAA	733		
DB	2	CACCTGGCTTCTCATTAAGTGAATGATGATCAATAATTTGGCAGAAGACCGTGAA	61		
QY	734	AGTACACAGCCGCTGTCAGTAGCACAAGAAACAAGAACTGTGCTAATGAGACTATA	793		
DB	62	AGTACACAGCCGCTGTCAGTAGCACAAGAAACAAGAACTGTGCTAATGAGACTATA	121		
QY	794	AATAACCTTAATAGCCATAGCATCTTCCATACCACTATCCCATTTTCAAGTATATT	853		
DB	122	AATAACCTTAATAGCCATAGCATCTTCCATACCACTATCCCATTTTCAAGTATATT	181		

RESULT 4
US-09-078-972A-22
; Sequence 22, Application US/09078972A
; Patent No. 6635806
; GENERAL INFORMATION:


```
; APPLICANT: KRIS, ALAN L.
; APPLICANT: LUTHEY, MICHAEL H.
; APPLICANT: VOYLES, DALE A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EXPRESSION OF TRANSGENES
; FILE OF INVENTION: IN PLANTS
; FILE REFERENCE: DEKM:158
; CURRENT APPLICATION NUMBER: US/09/078,972A
; CURRENT FILING DATE: 1998-05-14
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 2647
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
; US-09-078-972A-22
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Query Match          3.4%; Score 30; DB 4; Length 2647;
Best Local Similarity 100.0%; Pred. No. 2,4e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      522 GTAAAGTAATTTCACCAAGCCATATATCAA 551
Db      886 GTAAAGTAATTTCACCAAGCCATATATCAA 915
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```
RESULT 5
; US-09-078-972A-5
; Sequence 5, Application US/09078972A
; Patent No. 6635806
; GENERAL INFORMATION:
; APPLICANT: KRIS, ALAN L.
; APPLICANT: LUTHEY, MICHAEL H.
; APPLICANT: VOYLES, DALE A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EXPRESSION OF TRANSGENES
; FILE OF INVENTION: IN PLANTS
; FILE REFERENCE: DEKM:158
; CURRENT APPLICATION NUMBER: US/09/078,972A
; CURRENT FILING DATE: 1998-05-14
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
; US-09-078-972A-5
```

```
Query Match          2.6%; Score 23; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 GGACCGGTTACAGCACCACTG 23
Db      9 GGACCGGTTACAGCACCACTG 31
```

```
RESULT 6
; US-09-078-972A-12
; Sequence 12, Application US/09078972A
; Patent No. 6635806
; GENERAL INFORMATION:
; APPLICANT: KRIS, ALAN L.
; APPLICANT: LUTHEY, MICHAEL H.
; APPLICANT: VOYLES, DALE A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EXPRESSION OF TRANSGENES
; FILE OF INVENTION: IN PLANTS
; FILE REFERENCE: DEKM:158
; CURRENT APPLICATION NUMBER: US/09/078,972A
```

```
; CURRENT FILING DATE: 1998-05-14
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
; US-09-078-972A-12
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Query Match          2.6%; Score 23; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 GGACCGGTTACAGCACCACTG 23
Db      9 GGACCGGTTACAGCACCACTG 31
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RESULT 7
; US-09-949-016-30488/c
; Sequence 30488, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30488
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-30488
```

```
Query Match          2.5%; Score 22; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      815 CACTTCTCATACCACTACC 836
Db      138 CACTTCTCATACCACTACC 117
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```
RESULT 8
; US-09-949-016-179164/c
; Sequence 179164, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
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; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 179164
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-179164

Query Match
Best Local Similarity 100.0%; Score 22; DB 4; Length 601;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 815 CACTTCTCATCACCACCTACC 836
Db 138 CACTTCTCATCACCACCTACC 117

RESULT 9
US-09-949-016-12386/c
; Sequence 12386, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 12386
; LENGTH: 263693
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12386

Query Match
Best Local Similarity 100.0%; Score 22; DB 4; Length 263693;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 815 CACTTCTCATCACCACCTACC 836
Db 9163 CACTTCTCATCACCACCTACC 9142

RESULT 10
US-09-949-016-16915/c
; Sequence 16915, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 16915
; LENGTH: 263694
; TYPE: DNA
; ORGANISM: Human
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US-09-949-016-16915

Query Match
Best Local Similarity 100.0%; Score 22; DB 4; Length 263694;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 815 CACTTCTCATCACCACCTACC 836
Db 9163 CACTTCTCATCACCACCTACC 9142

RESULT 11
US-09-078-972A-6/c
; Sequence 6, Application US/09078972A
; Patent No. 6635806
; GENERAL INFORMATION:
; APPLICANT: KRIS, ALAN L.
; APPLICANT: LUEBTH, MICHAEL H.
; APPLICANT: VOYLES, DALE A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EXPRESSION OF TRANSGENES
; FILE REFERENCE: DEKM:158
; CURRENT APPLICATION NUMBER: US/09/078,972A
; CURRENT FILING DATE: 1998-05-14
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-078-972A-6

Query Match
Best Local Similarity 100.0%; Score 21; DB 4; Length 29;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 874 AGACGACGAAAGATCGACACC 894
Db 29 AGACGACGAAAGATCGACACC 9

RESULT 12
US-09-078-972A-7/c
; Sequence 7, Application US/09078972A
; Patent No. 6635806
; GENERAL INFORMATION:
; APPLICANT: KRIS, ALAN L.
; APPLICANT: LUEBTH, MICHAEL H.
; APPLICANT: VOYLES, DALE A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EXPRESSION OF TRANSGENES
; FILE REFERENCE: DEKM:158
; CURRENT APPLICATION NUMBER: US/09/078,972A
; CURRENT FILING DATE: 1998-05-14
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-078-972A-7

Query Match
Best Local Similarity 100.0%; Score 21; DB 4; Length 29;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 874 AGACGACGAAAGATCGACACC 894
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Db 29 AGACGACGAGATGACACC 9

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RESULT 13
US-09-949-016-11758
; Sequence 11758, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11758
; LENGTH: 32798
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11758

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Query Match 2.2%; Score 20; DB 4; Length 32798;
 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 699 TGATGAGTCATTAATATTG 718
 Db 8044 TGATGAGTCATTAATATTG 8063

```

RESULT 14
US-09-949-016-17366
; Sequence 17366, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17366
; LENGTH: 32798
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17366

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Query Match 2.2%; Score 20; DB 4; Length 32798;
 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 699 TGATGAGTCATTAATATTG 718
 Db 8044 TGATGAGTCATTAATATTG 8063

RESULT 15

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US-09-949-016-16297
; Sequence 16297, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16297
; LENGTH: 42118
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1) --(42118)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16297

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Query Match 2.2%; Score 20; DB 4; Length 42118;
 Best Local Similarity 100.0%; Pred. No. 3.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 459 AAAGTTGTTTCATGAAGAAA 478
 Db 368901 AAAGTTGTTTCATGAAGAAA 368920

Search completed: September 24, 2005, 19:28:02
 Job time : 200 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 24, 2005, 17:17:53 : Search time 670 Seconds
(without alignments)
8921.532 Million cell updates/sec

Title: US-10-660-097-8
Perfect score: 894
Sequence: 1 gggccgggttcacgacaccca.....gggcacagaagatccacacc 894

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 7400704 seqs, 3343079526 residues

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Total number of hits satisfying chosen parameters: 14801408

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Published Applications NA:*

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11: /cgn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/prodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/prodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/prodata/2/pubpna/US10E_PUBCOMB.seq:*
17: /cgn2_6/prodata/2/pubpna/US10F_PUBCOMB.seq:*
18: /cgn2_6/prodata/2/pubpna/US10G_PUBCOMB.seq:*
19: /cgn2_6/prodata/2/pubpna/US10H_PUBCOMB.seq:*
20: /cgn2_6/prodata/2/pubpna/US10I_PUBCOMB.seq:*
21: /cgn2_6/prodata/2/pubpna/US10J_NEW_PUB.seq:*
22: /cgn2_6/prodata/2/pubpna/US11_PUBCOMB.seq:*
23: /cgn2_6/prodata/2/pubpna/US11A_PUBCOMB.seq:*
24: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	20	2.2	724	13	US-10-027-632-26673
2	20	2.2	724	17	US-10-027-632-26673
3	20	2.2	1282	18	US-10-425-114-10169
4	20	2.2	1496	18	US-10-425-114-12726
5	20	2.2	2682	18	US-10-425-114-8803
6	20	2.2	2706	18	US-10-424-599-56507
7	20	2.2	2722	18	US-10-425-114-29746

C 8	20	2.2	3504	19	US-10-437-963-38619	Sequence 38619, A
C 9	20	2.2	4722	18	US-10-424-599-56505	Sequence 56505, A
C 10	20	2.2	495269	17	US-10-398-221-8	Sequence 8, App11
C 11	20	2.2	3011208	17	US-10-398-221-2058	Sequence 2058, Ap
C 12	19	2.1	196	19	US-10-767-701-23531	Sequence 23531, A
C 13	19	2.1	299	19	US-10-674-124A-5147	Sequence 5147, Ap
C 14	19	2.1	334	18	US-10-621-901-707	Sequence 707, App
C 15	19	2.1	400	17	US-10-242-535A-8147	Sequence 8147, Ap
C 16	19	2.1	400	18	US-10-085-783A-8147	Sequence 8147, Ap
C 17	19	2.1	497	9	US-09-864-761-2138	Sequence 2138, Ap
C 18	19	2.1	506	18	US-10-424-599-2019	Sequence 2019, Ap
C 19	19	2.1	516	20	US-10-653-047-6178	Sequence 6178, Ap
C 20	19	2.1	673	15	US-10-328-063-12	Sequence 12, App1
C 21	19	2.1	687	24	US-11-074-522-13	Sequence 13, App1
C 22	19	2.1	924	18	US-10-425-114-20405	Sequence 20405, A
C 23	19	2.1	1221	21	US-10-472-928-803	Sequence 803, App
C 24	19	2.1	1311	22	US-10-617-320-1216	Sequence 1216, Ap
C 25	19	2.1	1503	14	US-10-198-846-13111	Sequence 13111, A
C 26	19	2.1	1510	24	US-11-011-526A-26	Sequence 26, App1
C 27	19	2.1	1510	24	US-11-063-325-26	Sequence 26, App1
C 28	19	2.1	1625	17	US-10-104-047-1383	Sequence 1383, Ap
C 29	19	2.1	4848	21	US-10-489-740-2	Sequence 2, App11
C 30	19	2.1	5290	24	US-11-074-522-18	Sequence 18, App1
C 31	19	2.1	5912	24	US-11-074-522-16	Sequence 16, App1
C 32	19	2.1	7001	8	US-08-961-527-88	Sequence 88, App1
C 33	19	2.1	7001	17	US-10-158-844-88	Sequence 88, App1
C 34	19	2.1	7794	24	US-11-057-062-2	Sequence 2, App11
C 35	19	2.1	11357	24	US-11-074-522-14	Sequence 14, App1
C 36	19	2.1	11888	24	US-11-074-522-17	Sequence 17, App1
C 37	19	2.1	73507	13	US-10-087-192-1147	Sequence 1147, Ap
C 38	19	2.1	2162508	21	US-10-472-928-4879	Sequence 4879, Ap
C 39	18	2.0	431	18	US-10-333-184-387	Sequence 387, App
C 40	18	2.0	472	21	US-10-825-692-103	Sequence 103, App
C 41	18	2.0	506	9	US-09-864-761-11947	Sequence 11947, A
C 42	18	2.0	522	9	US-09-736-457-304	Sequence 304, App
C 43	18	2.0	522	9	US-09-902-941-304	Sequence 304, App
C 44	18	2.0	522	9	US-09-849-626-304	Sequence 304, App
C 45	18	2.0	522	10	US-09-476-300-304	Sequence 304, App

ALIGNMENTS

RESULT 1
US-10-027-632-26673
Sequence 26673, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26673
LENGTH: 724
TYPE: DNA

Query Match 2.2%: Score 20; DB 18; Length 2682;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 CTTGTTGGAAGCATAGCAGT 182
|||||
Db 1504 CTTGTTGGAAGCATAGCAGT 1485

RESULT 6

US-10-424-599-56507/c
; Sequence 56507, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 56507
; LENGTH: 2706
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_22035C.1
US-10-424-599-56507

Query Match 2.2%: Score 20; DB 18; Length 2706;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 CTTGTTGGAAGCATAGCAGT 182
|||||
Db 1528 CTTGTTGGAAGCATAGCAGT 1509

RESULT 7

US-10-425-114-29746/c
; Sequence 29746, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaka, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 29746
; LENGTH: 2722
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: uc-gmrominsoy315f07_FLI
US-10-425-114-29746

Query Match 2.2%: Score 20; DB 18; Length 2722;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 CTTGTTGGAAGCATAGCAGT 182
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Db 163 CTTGTTGGAAGCATAGCAGT 182

Db 1543 CTTGTTGGAAGCATAGCAGT 1524

RESULT 8

US-10-437-963-38619/c
; Sequence 38619, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 38619
; LENGTH: 3504
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_42239C.1
US-10-437-963-38619

Query Match 2.2%: Score 20; DB 19; Length 3504;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 CAAGCAGTACCAACTATA 53
|||||
Db 1740 CAAGCAGTACCAACTATA 1721

RESULT 9

US-10-424-599-56505/c
; Sequence 56505, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 56505
; LENGTH: 4722
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(4722)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_22033C.1
US-10-424-599-56505

Query Match 2.2%: Score 20; DB 18; Length 4722;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 CTTGTTGGAAGCATAGCAGT 182
|||||
Db 2483 CTTGTTGGAAGCATAGCAGT 2464


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RESULT 10
US-10-398-221-8/c
; Sequence 8, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 495269
; TYPE: DNA
; ORGANISM: Listeria innocua
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(end)
; OTHER INFORMATION: n can be any nucleotide: a, g, c or t/u
US-10-398-221-8

Query Match          2.2%; Score 20; DB 17; Length 495269;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      468 TTCATGAAAAACAATPAG 487
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Db      160350 TTCATGAAAAACAATPAG 160331

RESULT 11
US-10-398-221-2058
; Sequence 2058, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2058
; LENGTH: 3011208
; TYPE: DNA
; ORGANISM: Listeria innocua
US-10-398-221-2058

Query Match          2.2%; Score 20; DB 17; Length 3011208;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: KOVALIC, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21 (53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 23531
; LENGTH: 196
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 15545854
US-10-767-701-23531
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Query Match          2.1%; Score 19; DB 19; Length 196;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      576 TATATATACGCACGATGAT 594
      |||||||||||||||||||
Db      103 TATATATACGCACGATGAT 85
```

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RESULT 13
US-10-674-124A-5147
; Sequence 5147, Application US/10674124A
; Publication No. US2004019797A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: TAMURA, Gen
; TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE
; FILE REFERENCE: ORIN-003CIP
; CURRENT APPLICATION NUMBER: US/10/674,124A
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 10/257,511
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/JP00/07621
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: JP2000-112699
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: JP2002-327516
; PRIOR FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: JP2002-383869
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 27110
; SEQ ID NO 5147
; LENGTH: 299
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: D3S3577
; OTHER INFORMATION: Located on chromosome 3
; FEATURE:
; OTHER INFORMATION: Distance between a terminus base of telomere on
; OTHER INFORMATION: chromosomal short arm and 5'-terminus of this base
; FEATURE:
; OTHER INFORMATION: sequence : 62581159
; OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
; OTHER INFORMATION: sequence listing upward to telomere on chromosomal short arm and
; OTHER INFORMATION: 5'-terminus of this base sequence : 114938
US-10-674-124A-5147
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Query Match          2.1%; Score 19; DB 19; Length 299;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 468 TTCATGAAAAAACAAATA 486
 Db 40 TTCATGAAAAAACAAATA 58

RESULT 14

US-10-621-901-707
 ; Sequence 707, Application US/10621901
 ; Publication No. US20040067516A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brandt, Kevin S.
 ; APPLICANT: Gaines, Patrick J.
 ; APPLICANT: Stinchcomb, Dan T.
 ; APPLICANT: Wisniewski, Nancy
 ; TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE NUCLEIC ACID
 ; TITLE OF INVENTION: MOLECULES, PROTEINS AND USES THEREOF
 ; FILE REFERENCE: FC-8-C3
 ; CURRENT APPLICATION NUMBER: US/10/621,901
 ; CURRENT FILING DATE: 2003-07-17
 ; PRIOR APPLICATION NUMBER: 60/319,414
 ; NUMBER OF SEQ ID NOS: 2313
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 707
 ; LENGTH: 334
 ; TYPE: DNA
 ; ORGANISM: Ctenocephalides felis
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (5)..(5)
 ; OTHER INFORMATION: n = unknown
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (41)..(41)
 ; OTHER INFORMATION: n = unknown
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (47)..(47)
 ; OTHER INFORMATION: n = unknown
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (62)..(62)
 ; OTHER INFORMATION: n = unknown
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (95)..(95)
 ; OTHER INFORMATION: n = unknown
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (100)..(101)
 ; OTHER INFORMATION: n = unknown
 ; US-10-621-901-707

Query Match 2.1%; Score 19; DB 18; Length 334;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 298 TCACAAATTCACGCTCAA 316
 Db 20 TCACAAATTCACGCTCAA 38

RESULT 15

US-10-242-535A-8147/C
 ; Sequence 8147, Application US/10242535A
 ; Publication No. US20040013663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ChondroGene Inc.
 ; APPLICANT: Liew, C.C.
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
 ; FILE REFERENCE: 4231/2005
 ; CURRENT APPLICATION NUMBER: US/10/242,535A
 ; CURRENT FILING DATE: 2002-09-12

; PRIOR APPLICATION NUMBER: US 10/085,783
 ; PRIOR FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 60/305,340
 ; PRIOR FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: US 60/275,017
 ; PRIOR FILING DATE: 2001-03-12
 ; PRIOR APPLICATION NUMBER: US 60/271,955
 ; PRIOR FILING DATE: 2001-02-28
 ; NUMBER OF SEQ ID NOS: 58994
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 8147
 ; LENGTH: 400
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (396)..(396)
 ; OTHER INFORMATION: n is a, c, g, or t
 ; US-10-242-535A-8147

Query Match 2.1%; Score 19; DB 17; Length 400;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 338 CGTCTCCTGTAGCTTGTGA 356
 Db 249 CGTCTCCTGTAGCTTGTGA 231

Search completed: September 24, 2005, 19:39:29
 Job time : 679 secs

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